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(54) **POLYPEPTIDES DE 3-CETOACYL COA SYNTHASE, ELONGASE D'ACIDES GRAS**
(54) **FATTY ACID ELONGASE 3-KETOACYL COA SYNTHASE POLYPEPTIDES**



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(57) **Abrégé/Abstract:**

Elongase KCS polypeptides with altered substrate specificity and/or catalytic activity are disclosed. Such elongase KCS polypeptides are effective for producing very long chain fatty acids (VLCFA) fatty acids. Also disclosed are nucleic acids encoding elongase KCS polypeptides, and yeast and plants expressing these polypeptides.

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(54) Title: FATTY ACID ELONGASE 3-KETOACYL CoA SYNTHASE POLYPEPTIDES

(57) Abstract: Elongase KCS polypeptides with altered substrate specificity and/or catalytic activity are disclosed. Such elongase KCS polypeptides are effective for producing very long chain fatty acids (VLCFA) fatty acids. Also disclosed are nucleic acids encoding elongase KCS polypeptides, and yeast and plants expressing these polypeptides.

Fatty Acid Elongase 3-Ketoacyl CoA Synthase Polypeptides

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority under 35 U.S.C. §119(e) of U.S. provisional application serial number 60/210,326, filed June 8, 2000.

5

TECHNICAL FIELD

This invention relates to enzymes involved in very long chain fatty acid (VLCFA) synthesis, and more particularly to chimeras and mutants of nucleic acid sequences encoding fatty acid elongase 3-ketoacyl CoA synthase polypeptides.

BACKGROUND

10 Plant seeds accumulate primarily 16- and 18-carbon fatty acids (FA). Plants also synthesize very long chain fatty acids (VLCFA). VLCFAs are saturated or unsaturated monocarboxylic acids with an unbranched even-numbered carbon chain that is greater than 18 carbons in length. Very long chain fatty acids are key components of many biologically important compounds in animals, plants, and microorganisms. For example, 15 in animals, the VLCFA arachidonic acid is a precursor to many prostaglandins. In plants, VLCFAs are major constituents of triacylglycerols in many seed oils, are essential precursors for cuticular wax production, and are utilized in the synthesis of glycosylceramides, a component of the plasma membrane. Important VLCFAs include arachidic acid (C20:0; *i.e.*, a 20 carbon chain with no double bonds), behenic acid 20 (C22:0), erucic acid (C22:1), and lignoceric acid (C24:1).

VLCFAs are not desirable in edible oils. Oilseeds of the *Crucifereae* (*e.g.*, rapeseed) and a few other plants, however, accumulate C20 and C22 fatty acids. Although plant breeders have developed rapeseed lines that have low levels of VLCFAs for edible oil purposes, even lower levels would be desirable. On the other hand, 25 vegetable oils having elevated levels of VLCFAs are desirable for certain industrial uses, including uses as lubricants, fuels and as a feedstock for plastics, pharmaceuticals and cosmetics.

The biosynthesis in plants of saturated fatty acids up to an 18-carbon chain occurs in the chloroplast. C2 units from acyl thioesters are linked sequentially, beginning with the condensation of acetyl Co-enzyme A (CoA) and malonyl-acyl carrier protein (malonyl-ACP) to form a C4 acyl fatty acid. This condensation reaction is catalyzed by a 3-ketoacyl synthase III (KASIII). The enzyme 3-ketoacyl synthase I (KASI) catalyzes the stepwise condensation of a fatty acyl moiety (C4 to C14) with C2 groups and malonyl-ACP to produce a 3-ketoacyl-ACP product that is 2 carbons longer than the original substrate (C6 to C16). The last condensation reaction in the chloroplast, converting C16 to C18, is catalyzed by 3-ketoacyl synthase II (KASII). 3-ketoacyl moieties are also referred to as β -ketoacyl moieties.

Each elongation cycle involves three additional enzymatic steps in addition to the condensation reaction discussed above. Briefly, the 3-ketoacyl condensation product is reduced to 3-hydroxyacyl-ACP, dehydrated to the enoyl-ACP, and reduced to an acyl-ACP. The fully reduced fatty acyl-ACP reaction product then serves as the substrate for the next cycle of elongation.

The C18:0 saturated fatty acid (stearic acid) can be desaturated to produce a C18:1 fatty acid (oleic acid), which can be transported out of the chloroplast and converted to a C18:2 fatty acid (linoleic acid) or a C18:3 fatty acid (α -linolenic acid). Stearic acid and oleic acid can also be elongated outside the chloroplast to form VLCFAs. The formation of fatty acids longer than 18 carbons depends on the activity of a fatty acid elongase complex to carry out four reactions similar to those described above for fatty acid synthesis in the chloroplast. The initial reaction is catalyzed by an elongase 3-ketoacyl CoA synthase (elongase KCS) and involves the condensation of a two carbon group from malonyl CoA with a C18:0 or C18:1 fatty acyl CoA substrate. A gene encoding an elongase KCS from *Arabidopsis thaliana* has been identified and designated *FAE1*. See, e.g., U.S. Patent No. 6,124,524. The gene product catalyzes the condensation of oleoyl CoA and malonyl CoA, leading to the conversion of the C18 substrate to a C20:1 product, eicosenoyl CoA. Mutations have been identified in the *A. thaliana* *FAE1* gene (see WO 96/13582). *A. thaliana* plants carrying a mutation in *FAE1* have significant decreases in the levels of VLCFAs in seeds.

SUMMARY

Despite 85% sequence identity at the amino acid level between the *Arabidopsis thaliana* FAE1 polypeptide and the *Brassica napus* polypeptide of GenBank Accession No. AAB72178, the composition of the oil from *A. thaliana* and *B. napus* seeds suggests
5 that the enzymes may have different substrate specificities and/or catalytic activity. VLCFAs constitute about 22% of the seed oil of *A. thaliana*, whereas VLCFAs constitute about 62% of the seed oil in rape. *A. thaliana* seed oil is primarily eicosenoic acid (about 18%), with a small amount of erucic acid and longer-chain monounsaturated fatty acids (about 2%). In contrast, rapeseed oil has a relatively small amount of eicosenoic acid
10 (about 10%) and relatively larger amounts of erucic acid and longer-chain monunsaturates (about 52%).

The present invention provides novel polypeptides with altered elongase KCS substrate specificity and/or catalytic activity. One such novel polypeptide comprises three polypeptide segments. The amino-terminal first polypeptide segment has
15 membrane-anchoring properties. It is joined to a second polypeptide segment whose amino acid sequence is residues 75-114 of SEQ ID NO:12 or residues 75-114 of SEQ ID NO:14, followed by a third polypeptide segment having at least 40% sequence identity to the C-terminal 392 amino acids of SEQ ID NO:4. Examples of such polypeptides have the amino acid sequences shown in SEQ ID NOS:12 and 14. The third polypeptide
20 segment can have an aspartic acid residue at the position corresponding to amino acid 307 of SEQ ID NO:4. Examples of such polypeptides have the amino acid sequences shown in SEQ ID NOS:20, 22, 34 and 36.

Such polypeptides can catalyze the condensation of a C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of a C20 fatty acyl CoA. The fatty acid substrate
25 can be oleic acid (C18:1), in which case the product formed is eicosenoic acid (C20:1). In some instances, the fatty acid substrate is stearic acid (C18:0) and the product formed therefrom is arachidic acid (C20:0). Such polypeptides often can further catalyze the condensation of malonyl CoA and a C20 fatty acyl substrate, leading to the synthesis of a C22 fatty acyl CoA. The substrate often is eicosenoic acid (C20:1) and the product is
30 erucic acid (C22:1).

The ratio of the C22 fatty acid product to the C20 fatty acid product (C22:1/C20:1) resulting from the activity of such polypeptides can be about 0.20 or greater, about 0.30 or greater, about 0.40 or greater, or about 0.50 or greater as measured in a yeast microsome assay.

5 The invention also features a polypeptide comprising in the amino-terminal to carboxy-terminal direction: a first polypeptide segment that has membrane anchoring properties, joined to a second polypeptide segment that has residues 75-114 of SEQ ID NO:2, which is in turn joined to a third polypeptide segment that has at least 90% sequence identity to residues 115-506 of SEQ ID NO:4. An example of such a
10 polypeptide has the amino acid sequence of SEQ ID NO:8. Also featured is a polypeptide comprising in the amino-terminal to carboxy-terminal direction: a first polypeptide segment having at least 80% sequence identity to residues 1-74 of SEQ ID NO:2, joined to a second polypeptide segment having residues 76-114 of SEQ ID NO:4, joined to a third polypeptide segment having at least 40% sequence identity to residues 115-506 of
15 SEQ ID NO:4. An example of such a polypeptide has the amino acid sequence of SEQ ID NO:10. In some embodiments of these polypeptides, the third segment has an aspartic acid at the position corresponding to amino acid 307 of said SEQ ID NO:4. Examples of such polypeptides have the amino acid sequences of SEQ ID NO:16 and SEQ ID NO:18.

 A plant is also disclosed, comprising at least one exogenous nucleic acid encoding
20 one or more of the novel polypeptides disclosed herein, as well as seeds having such nucleic acids.

 Nucleic acid constructs of the invention comprise at least one regulatory element operably linked to the nucleic acid coding sequence for a novel polypeptide. Host cells containing such nucleic acid constructs are disclosed. Such host cells include bacterial
25 cells, fungal cells, insect cells, plant cells and animal cells.

 A method of altering very long chain fatty acids in an organism is disclosed. The method comprises introducing an exogenous nucleic acid into the organism. The nucleic acid encodes one or more of the polypeptides described herein. The nucleic acid is expressed in the organism to produce the polypeptide(s), and the very long chain fatty
30 acid content of the organism is increased compared to the very long chain fatty acid content of a corresponding organism that lacks the exogenous nucleic acid or does not

express the exogenous nucleic acid. Suitable organisms include fungi (e.g., yeast), plants, animals, insects and bacteria. Such organisms can produce a higher level of erucic acid than a corresponding organism that lacks or does not express the exogenous nucleic acid.

Unless otherwise defined, all technical and scientific terms used herein have the
5 same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. For example, the one letter and three letter abbreviations for amino acids and the one-letter abbreviations for nucleotides are commonly understood. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are
10 described below. In addition, the materials, methods and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

The details of one or more embodiments of the invention are set forth in the
15 accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the drawings and detailed description, and from the claims.

BRIEF DESCRIPTION OF SEQUENCES

20 SEQ ID NO:1 is the nucleotide sequence of the *Arabidopsis thaliana* FAEI gene (GenBank Accession No. U29142).

SEQ ID NO:2 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:1 (GenBank Accession No. AAA70154).

25 SEQ ID NO:3 is the nucleotide sequence of a *Brassica napus* fatty acid elongase KCS (GenBank Accession No. AF009563).

SEQ ID NO:4 is the amino acid sequence of the *B. napus* polypeptide encoded by SEQ ID NO:3 (GenBank Accession No. AAB72178).

SEQ ID NO:5 is the nucleotide sequence of a *B. napus* fatty acid elongase KCS (GenBank Accession No. U50771).

30 SEQ ID NO:6 is the amino acid sequence of the *B. napus* polypeptide encoded by SEQ ID NO:5 (GenBank Accession No. AAA96054).

SEQ ID NO:7 is a nucleotide sequence encoding a polypeptide designated At114.

SEQ ID NO:8 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:7.

SEQ ID NO:9 is a nucleotide sequence encoding a polypeptide designated At74.

5 SEQ ID NO:10 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:9.

SEQ ID NO:11 is a nucleotide sequence encoding a polypeptide designated At114 L91C K92R.

SEQ ID NO:12 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:11.

10 SEQ ID NO:13 is a nucleotide sequence encoding a polypeptide designated At114 K92R.

SEQ ID NO:14 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:13.

15 SEQ ID NO:15 is a nucleotide sequence encoding a polypeptide designated At114 G307D.

SEQ ID NO:16 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:15.

SEQ ID NO:17 is a nucleotide sequence encoding a polypeptide designated At74 G306D.

20 SEQ ID NO:18 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:17.

SEQ ID NO:19 is a nucleotide sequence encoding a polypeptide designated At114 L91C K92R G307D.

25 SEQ ID NO:20 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:19.

SEQ ID NO:21 is a nucleotide sequence encoding a polypeptide designated At114 K92R G307D.

SEQ ID NO:22 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:21.

30 SEQ ID NO:23 is a nucleotide sequence encoding a polypeptide designated At254.

SEQ ID NO:24 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:23.

SEQ ID NO:25 is a nucleotide sequence encoding a polypeptide designated At173.

5 SEQ ID NO:26 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:25.

SEQ ID NO:27 is a nucleotide sequence encoding a polypeptide designated Bn176.

10 SEQ ID NO:28 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:27.

SEQ ID NO:29 is a nucleotide sequence encoding a polypeptide designated At399.

SEQ ID NO:30 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:29.

15 SEQ ID NO:31 is a nucleotide sequence encoding a polypeptide designated Bn399.

SEQ ID NO:32 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:31.

20 SEQ ID NO:33 is a nucleotide sequence encoding a polypeptide designated Bn G307D.

SEQ ID NO:34 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:33.

SEQ ID NO:35 is a nucleotide sequence encoding a polypeptide designated At K92R.

25 SEQ ID NO:36 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:35.

SEQ ID NO:37 is a nucleotide sequence encoding a polypeptide designated At254 G307D.

30 SEQ ID NO:38 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:37.

SEQ ID NO:39 is a nucleotide sequence encoding a polypeptide designated At173 G307D.

SEQ ID NO:40 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:39.

5 SEQ ID NO:41 is a nucleotide sequence encoding a polypeptide designated Bn399 G307D.

SEQ ID NO:42 is the amino acid sequence of the polypeptide encoded by SEQ ID NO:41.

10 SEQ ID NO:43 is the 3' chimera-specific primer used in the generation of At173.

SEQ ID NO:44 is the 5' chimera-specific primer used in the generation of At173.

SEQ ID NO:45 is the 3' chimera-specific primer used in the generation of At114.

SEQ ID NO:46 is the 5' chimera-specific primer used in the generation of At114.

SEQ ID NO:47 is the 3' chimera-specific primer used in the generation of At74.

SEQ ID NO:48 is the 5' chimera-specific primer used in the generation of At74.

15 SEQ ID NO:49 is the 3' chimera-specific primer used in the generation of At114 L91C K92R.

SEQ ID NO:50 is the 5' chimera-specific primer used in the generation of At114 L91C K92R.

20 SEQ ID NO:51 is the 3' chimera-specific primer used in the generation of At114 K92R.

SEQ ID NO:52 is the 5' chimera-specific primer used in the generation of At114 K92R.

SEQ ID NO:53 is the 5' universal primer used in the generation of At-Bn chimeras.

25 SEQ ID NO:54 is the 3' universal primer used in the generation of At-Bn chimeras.

SEQ ID NO:55 is the 5' universal primer used in the generation of Bn-At chimeras.

30 SEQ ID NO:56 is the 3' universal primer used in the generation of Bn-At chimeras.

DESCRIPTION OF DRAWINGS

Figure 1 shows amino acid sequences of *Brassica napus* (Bn) elongase KCS polypeptides, *Arabidopsis thaliana* FAE1 (At) and novel chimeric polypeptides and novel chimeric polypeptides containing site-directed modifications. Sequences corresponding to those derived from At FAE1 are underlined. Site-directed modifications are indicated in bold. One of the Bn elongase KCS sequences shown corresponds to GenBank Accession No. AAB72178; the other *B. napus* sequence shown corresponds to a second *B. napus* elongase KCS having GenBank Accession No. AAA96054.

Figure 2 shows nucleotide sequences of Bn elongase KCS, At *FAE1* and novel chimeric nucleic acids and novel chimeric nucleic acids containing site-directed modifications. Sequences corresponding to those derived from At *FAE1* are underlined. Site-directed modifications are indicated in bold. The two Bn elongase KCS nucleic acid sequences shown encode the two Bn polypeptides shown in Fig. 1. The GenBank Accession Numbers are AF009563 and U50771, respectively.

Like reference symbols in the various drawings indicate like elements.

DETAILED DESCRIPTION

Fatty Acid Elongase KCS Polypeptides

In one aspect, the invention provides a polypeptide containing the following segments in the amino-terminal to carboxy-terminal direction: a first polypeptide segment having membrane anchoring properties, joined to a second polypeptide segment having the amino acid sequence of residues of 75-114 of SEQ ID NO:12 or SEQ ID NO:14, joined to a third polypeptide segment having at least 40% sequence identity to the C-terminal approximately 392 amino acids of the *Brassica napus* elongase KCS polypeptide shown in SEQ ID NO:4. For example, polypeptides designated At114 L91C K92R (SEQ ID NO:12) and At114 K92R (SEQ ID NO:14) are provided by the present invention. The primary sequence of the novel polypeptides of the invention are identified by the source and number of amino-terminal residues (*e.g.*, At74 polypeptides have 74 amino-terminal residues from *Arabidopsis thaliana*), and site-directed modifications are indicated by the

original amino acid residue, the position of the modification and the new residue (*e.g.*, polypeptides containing a K92R site-directed modification had a K at amino acid position 92 which was modified by site-directed mutagenesis of the nucleic acid to encode an R residue).

5 The above-described polypeptides include a first polypeptide segment that can serve as a membrane anchor. Such a segment has properties that result in the elongase KCS polypeptide being anchored to a membrane, such as a lipid bilayer, detergent bilayer, micelle, or cell membrane. Possession of membrane anchoring properties may be the result of the primary structure, secondary structure and/or tertiary structure of the
10 segment. For example, the segment may contain one or more transmembrane domain(s). Alternatively, a post-translational modification of an amino acid residue within the segment can result in the polypeptide being anchored to a membrane. Suitable modifications include, but are not limited to, covalent attachment of a lipid (*e.g.*, a glycosyl phosphatidylinositol anchor) or a carbohydrate (*e.g.*, an oligosaccharide). See,
15 Alberts et al., *The Cell*, 2nd Edition, Garland Publishing, New York, pp 284-298 and Lodish et al., *Molecular Cell Biology*, 3rd Edition, Scientific American Books, p. 604 and pp. 688-692. The ability of a segment to serve as a membrane anchor can be demonstrated by observing whether a polypeptide having such a segment co-purifies with a membrane fraction. Alternatively, a segment can be a membrane-anchor if, after fusing
20 it to the second and third segments, it is shown that the polypeptide possesses elongase KCS activity in an *in vitro* yeast microsome assay, since elongase KCS polypeptides are active when anchored to a membrane. As another alternative, computer algorithms, such as Predict Protein or META Predict Protein (see www.embl-heidelberg.de/predictprotein), can be used to predict the presence of a transmembrane
25 domain within a segment, and hence, the ability of that polypeptide segment to serve as a membrane anchor.

 Examples of polypeptide segments that can be membrane anchors include, but are not limited to, amino acids 1-74 of *A. thaliana* FAE1 (SEQ ID NO:2), and amino acid sequences having 40% or greater sequence identity to residues 1-74 of SEQ ID NO:2.

30 For example, amino acids 1-75 of an elongase KCS from *B. napus* (GenBank Accession No. AAB72178), amino acids 1-75 of *B. juncea* protein (EMBL Accession No.

CAA71898), amino acids 1-75 of an elongase KCS from *B. napus* (GenBank Accession No. AAA96054), amino acids 29-105 of a putative β -ketoacyl-CoA synthase from *A. thaliana* (GenBank Accession No. AAD22309) and amino acids 8-76 of a fatty acid elongase-like protein from *A. thaliana* (EMBL Accession No. CAB36702) have at least
5 40% sequence identity to SEQ ID NO:2. In some embodiments, the first polypeptide segment has at least 80% sequence identity, 90% sequence identity, at least 95% sequence identity, or at least 99% sequence identity to amino acids 1-74 of SEQ ID NO:2.

A percent identity for any subject nucleic acid or amino acid sequence (*e.g.*, any of the fatty acid elongase chimeras described herein) relative to another "target" nucleic
10 acid or amino acid sequence can be determined as follows. First, a target nucleic acid or amino acid sequence of the invention can be compared and aligned to a subject nucleic acid or amino acid sequence, preferably using the BLAST 2 Sequences (B12seq) program from the stand-alone version of BLASTZ containing BLASTN and BLASTP (*e.g.*, version 2.0.14). The stand-alone version of BLASTZ can be obtained at <www.fr.com>
15 or <www.ncbi.nlm.nih.gov>. Instructions explaining how to use BLASTZ, and specifically the B12seq program, can be found in the 'readme' file accompanying BLASTZ. The programs also are described in detail by Karlin et al. (*Proc. Natl. Acad. Sci. USA*, 87:2264 (1990) and 90:5873 (1993)) and Altschul et al. (*Nucl. Acids Res.*, 25:3389 (1997)).

20 B12seq performs a comparison between the subject sequence and a target sequence using either the BLASTN (used to compare nucleic acid sequences) or BLASTP (used to compare amino acid sequences) algorithm. Typically, the default parameters of a BLOSUM62 scoring matrix, gap existence cost of 11, a per residue cost of 1 and a lambda ratio of 0.85 are used when performing amino acid sequence alignments. The
25 output file contains aligned regions of homology between the target sequence and the subject sequence. Once aligned, a length is determined by counting the number of consecutive nucleotides or amino acid residues (*i.e.*, excluding gaps) from the target sequence that align with sequence from the subject sequence starting with any matched position and ending with any other matched position. A matched position is any position
30 where an identical nucleotide or amino acid residue is present in both the target and subject sequence. Gaps of one or more residues can be inserted into a target or subject

sequence to maximize sequence alignments between structurally conserved domains (*e.g.*, α -helices, β -sheets, and loops).

The percent identity over a particular length is determined by counting the number of matched positions over that particular length, dividing that number by the length and multiplying the resulting value by 100. For example, if (i) a 1000 nucleotide target
5 sequence is compared to a subject nucleic acid sequence (*e.g.*, SEQ ID NO:21), (ii) the Bl2seq program presents 200 nucleotides from the target sequence aligned with a region of the subject sequence where the first and last nucleotides of that 200 nucleotide region are matches, and (iii) the number of matches over those 200 aligned nucleotides is 180,
10 then the 1000 nucleotide target sequence contains a length of 200 and a percent identity over that length of 90 (*i.e.*, $180 \div 200 \times 100 = 90$).

It will be appreciated that a nucleic acid or amino acid target sequence that aligns with a subject sequence can result in many different lengths with each length having its own percent identity. It is noted that the percent identity value can be rounded to the
15 nearest tenth. For example, 78.11, 78.12, 78.13, and 78.14 is rounded down to 78.1, while 78.15, 78.16, 78.17, 78.18, and 78.19 is rounded up to 78.2. It is also noted that the length value will always be an integer.

Polypeptides of the invention have a second segment which contains amino acid residues, in particular, the amino acid residue corresponding to position 92 in SEQ ID NO:2,
20 that affect elongase KCS substrate specificity. If the residue at position 92 is an arginine residue, the ratio of the C22:1 product to the C20:1 product is higher than the corresponding ratio observed when the residue is a lysine. Accordingly, the second segment (residues 75-114) of At114 L91C K92R and At114 K92R both possess an R at position 92. Another example of such a polypeptide has the amino acid sequence of SEQ ID NO:2, except that
25 the lysine at amino acid residue 92 is replaced with an arginine. This polypeptide, designated At K92R, has the amino acid sequence shown in SEQ ID NO:36.

Some polypeptides of the invention have a third segment that has at least 40% sequence identity to residues 115-506 of SEQ ID NO:4, which are the carboxy-terminal 392 amino acids of the *B. napus* polypeptide. In some embodiments, the third
30 polypeptide segment has at least 50% sequence identity, at least 60% sequence identity, at

least 70%, 80%, 90%, 95% or 99% sequence identity to the carboxy-terminal 392 amino acids of SEQ ID NO:4.

In some embodiments, the third segment has an aspartic acid residue at the position corresponding to amino acid residue 307 of SEQ ID NO:4. An aspartic acid residue at this position is useful for increasing the catalytic activity of an elongase KCS, compared to the catalytic activity of an otherwise similar polypeptide that has a glycine at this position. For example, polypeptides designated At114 G307D, At74 G306D, At114 L91C K92R G307D, At114 K92R G307D, At254 G307D, At173 G307D, Bn G307D and Bn399 G307D have an aspartic acid residue at the position corresponding to residue 307 of SEQ ID NO:4. These polypeptides have SEQ ID NOS: 16, 18, 20, 22, 38, 40, 34 and 42, respectively.

In some embodiments, the third segment contains one or more of the following groups of residues: GNTSSSS at positions corresponding to residues 423-429 of SEQ ID NO:4, HAGG(R/K)A at positions corresponding to residues 391-396 of SEQ ID NO:4, or MGCSAG at positions corresponding to residues 221-226 of SEQ ID NO:4. These groups of residues are among those that are conserved among elongase KCS polypeptides and are thus found in preferred embodiments.

Segments of a polypeptide are joined to one another by covalent bonds, typically peptide bonds. The segments can be joined directly, without any intervening residues between two segments. Alternatively, one segment can be joined indirectly to an adjacent segment by amino acid residues that are situated between the two adjacent segments and are themselves covalently joined to the adjacent segments. In some embodiments, there are one, two or three intervening amino acid residues. In other embodiments, there are four, five, six, seven, eight, nine or ten intervening residues.

A polypeptide of the invention optionally can possess additional amino acid residues at the amino-terminus or the carboxy-terminus. For example, six His-tag or FLAG™ residues may be linked to a polypeptide at the amino-terminus. See, *e.g.*, U.S. Patent Nos. 4,851,341 and 5,001,912. A reporter polypeptide, such as green fluorescent protein, may be fused to the carboxy-terminus. See, for example, U.S. Patent No. 5,491,084.

With respect to polypeptides, "isolated" refers to a polypeptide that constitutes the major component in a mixture of components, *e.g.*, 30% or more, 40% or more, 50% or more, 60% or more, 70% or more, 80% or more, 90% or more, or 95% or more by weight.

Isolated polypeptides typically are obtained by purification from an organism that makes
5 the polypeptide, although chemical synthesis is also feasible. As used herein, "enriched" refers to a polypeptide that constitutes 20-30% (by weight) of a mixture of components. Methods of polypeptide purification include, for example, chromatography or immunoaffinity techniques.

A polypeptide of the invention may be detected by sodium dodecyl sulphate
10 (SDS)-polyacrylamide gel electrophoresis followed by Coomassie Blue-staining or Western blot analysis using monoclonal or polyclonal antibodies that have binding affinity for the polypeptide to be detected.

The presence of a polypeptide of the invention may often be detected by measuring elongase KCS activity. An elongase KCS can catalyze the condensation of a
15 C18 fatty acyl substrate and malonyl CoA, leading to the formation of a C20 fatty acyl product. C18 fatty acids include C18:0 (*e.g.*, stearic acid), C18:1 (*e.g.*, oleic acid), C18:2 (*e.g.*, linoleic acid), and C18:3 (*e.g.*, α -linolenic acid). In some embodiments, an elongase KCS can catalyze the conversion of a C20 fatty acyl substrate to a C22 fatty acyl product. An example of a C20:1 fatty acyl substrate is an eicosenoyl substrate. Such a substrate
20 can be converted to a C22:1 fatty acyl product, *e.g.*, an erucyl product.

Some polypeptides may result in an elongase KCS that does not form reaction product(s) at a desired rate. Such elongases and their genes are useful as controls in analyses of product formation by enzymatically active elongase KCS polypeptides. Such inactive elongase KCS polypeptides and their genes can also be useful in studying the
25 regulation (*e.g.*, transcription, translation, and post-translational events) of genes encoding enzymatically active elongase KCS polypeptides. Such elongase KCS polypeptides can be attached to Sepharose beads and used for affinity purification of fatty acyl substrates from crude preparations. In addition, such elongase KCS polypeptides and their genes can also be useful to develop reagents for various purposes, *e.g.*,
30 immunological reagents to monitor expression of a elongase KCS polypeptides or nucleic

acid probes or primers to monitor inheritance of a elongase KCS gene in a plant breeding program.

Products formed in plants by elongase reactions involving an elongase KCS can be subsequently used to form fatty acyl triacylglycerides (TAGs) during seed
5 development. Alternatively, such products can be further elongated to form cuticular lipids, such as waxes.

In yet another aspect, the invention provides a polypeptide containing the following segments in the amino-terminal to carboxy-terminal direction: a first polypeptide segment having at least 80% sequence identity to the first 74 amino acids of
10 the *A. thaliana* *FAEI* gene product (SEQ ID NO:2), joined to a second polypeptide segment having amino acids 76-114 of SEQ ID NO:4, joined to a third polypeptide segment having at least 40% sequence identity to the C-terminal 392 amino acids of a *B. napus* elongase KCS (SEQ ID NO:4). An example of such a polypeptide is At74 (SEQ ID NO:10). This polypeptide possesses an R residue at position 92. Another example is
15 At74 G306D (SEQ ID NO:18), which has a D residue at position 306.

Another novel polypeptide disclosed herein contains the following segments in the amino-terminal to carboxy-terminal direction: a first polypeptide segment having membrane anchoring properties, joined to a second polypeptide segment corresponding to amino acids 75-114 of SEQ ID NO:2, joined to a third polypeptide segment having at
20 least 90% sequence identity to the C-terminal 392 amino acids of SEQ ID NO:4. An example of such a polypeptide is At114 (SEQ ID NO:8).

The invention also features the following polypeptide, comprising in the amino-terminal to carboxy-terminal direction: (a) a first polypeptide segment having at least 90% sequence identity to residues 1-254 of SEQ ID NO:2, joined to (b) a second
25 polypeptide segment having the amino acid sequence of residues 255-506 of SEQ ID NO:4. An example of such a polypeptide is designated At254 and the amino acid sequence is shown in Fig. 1 and SEQ ID NO:24.

Another novel polypeptide comprises (a) a first polypeptide segment having at least 85% sequence identity to residues 1-173 of SEQ ID NO:2, joined to (b) a second
30 polypeptide segment having the amino acid sequence of residues 174-506 of SEQ ID

NO:4. An example of such a polypeptide is designated At173 and the amino acid sequence is shown in Fig. 1 and SEQ ID NO:26.

Another novel polypeptide comprises: (a) a first polypeptide segment having at least 90% sequence identity to residues 1-399 of SEQ ID NO:2, joined to (b) a second polypeptide segment having amino acid residues 400-506 of SEQ ID NO:4. An example of such a polypeptide is designated At399 and the amino acid sequence is shown in Fig. 1 and SEQ ID NO:30. Such a polypeptide can exhibit a product ratio and catalytic activity resembling that of wild-type At FAE1.

The invention also features the following polypeptide, comprising in the amino-terminal to carboxy-terminal direction: (a) a first polypeptide segment having amino acid residues 1-176 of SEQ ID NO:4, joined to (b) a second polypeptide segment having at least 95% sequence identity to residues 177-506 of SEQ ID NO:2. An example of such a polypeptide is designated Bn176 and the amino acid sequence is shown in Fig. 1 and SEQ ID NO:28. In yeast microsome assays, the Bn176 polypeptide exhibits detectable elongase KCS catalytic activity and a C21:1/C20:1 product ratio of about 0.51.

The invention also features the following polypeptide, comprising in the amino-terminal to carboxy-terminal direction: (a) a first polypeptide segment having amino acid residues 1-399 of SEQ ID NO:4, joined to (b) a second polypeptide segment having at least 95% sequence identity to residues 400-506 of SEQ ID NO:2. An example of such a polypeptide is designated Bn399 and the amino acid sequence is shown in Fig. 1 and SEQ ID NO:32. In yeast microsome assays, the Bn399 polypeptide exhibits detectable elongase KCS catalytic activity and a C21:1/C20:1 product ratio of about 0.35.

Elongase KCS Nucleic Acids and Constructs

The present invention also includes nucleic acids encoding the above-described polypeptides. As used herein, nucleic acid refers to RNA or DNA, including cDNA, synthetic DNA or genomic DNA. The nucleic acids may be single- or double-stranded, and if single-stranded, may be either the coding or non-coding strand. As used herein with respect to nucleic acids, "isolated" refers to (i) a naturally-occurring nucleic acid encoding part or all of a polypeptide of the invention, but free of sequences, *i.e.*, coding sequences, that normally flank one or both sides of the nucleic acid encoding polypeptide

in a genome; (ii) a nucleic acid incorporated into a vector or into the genomic DNA of an organism such that the resulting molecule is not identical to any naturally-occurring vector or genomic DNA; or (iii) a cDNA, a genomic nucleic acid fragment, a fragment produced by polymerase chain reaction (PCR) or a restriction fragment. Specifically
5 excluded from this definition are nucleic acids present in mixtures of nucleic acid molecules or cells.

Examples of such nucleic acids include those encoding polypeptides designated At114, At74, At114 L91C K92R, At114 K92R, At114 G307D, At74 G306D, At114 L91C K92R G307D, At114 K92R G307D, At254, At173, Bn176, At399, Bn399 and At
10 K92R. These nucleic acids have SEQ ID NOS: 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 35, respectively. It should be appreciated that nucleic acids having a nucleotide sequence other than the specific nucleotide sequences disclosed can still encode a polypeptide having the exemplified amino acid sequence. The degeneracy of the genetic code is well known to the art; *i.e.*, for many amino acids, there is more than one
15 nucleotide triplet that serves as the codon for the amino acid.

Further provided are nucleic acid constructs comprising the above-described nucleic acid coding sequences. Such constructs may be incorporated into a cloning vector. Cloning vectors suitable for use in the present invention are commercially available and used routinely by those of ordinary skill. Nucleic acid constructs of the
20 invention may additionally comprise one or more regulatory elements operably linked to a nucleic acid coding sequence. Such regulatory elements may include promoter sequences, enhancer sequences, response elements or inducible elements that modulate expression of a nucleic acid sequence. As used herein, "operably linked" refers to positioning of a regulatory element in a construct relative to a nucleic acid coding
25 sequence in such a way as to permit or facilitate expression of the encoded polypeptide. The choice of element(s) that may be included depends upon several factors, including, but not limited to, replication efficiency, selectability, inducibility, targeting, the level of expression desired, ease of recovery and the ability of the host to perform post-translational modifications.

30 The term "host" or "host cell" includes not only prokaryotes, such as *E. coli*, but also eukaryotes, such as fungal, insect, plant and animal cells. Animal cells include, for

example, COS cells and HeLa cells. Fungal cells include yeast cells, such as *Saccharomyces cerevisiae* cells. A host cell can be transformed or transfected with a DNA molecule (e.g., a vector) using techniques known to those of ordinary skill in this art, such as calcium phosphate or lithium acetate precipitation, electroporation, lipofection and particle bombardment. Host cells containing a vector of the present invention may be used for such purposes as propagating the vector, producing a nucleic acid (e.g., DNA, RNA, antisense RNA) or expressing a polypeptide or fragments thereof.

A nucleic acid encoding a novel polypeptide of the invention may be obtained using standard molecular biology techniques, for example, molecular cloning, DNA synthesis, and the polymerase chain reaction (PCR). PCR refers to a procedure or technique in which target nucleic acids are amplified. PCR can be used to amplify specific sequences from DNA as well as RNA, including sequences from total genomic DNA or total cellular RNA. Various PCR methods are described, for example, in *PCR Primer: A Laboratory Manual*, Dieffenbach, C. & Dveksler, G., Eds., Cold Spring Harbor Laboratory Press, 1995. Generally, sequence information from the ends of the region of interest or beyond is employed to design oligonucleotide primers that are identical or similar in sequence to opposite strands of the template to be amplified. Various PCR strategies are available by which site-specific nucleotide sequence modifications can be introduced into a template nucleic acid.

Nucleic acids of the present invention may be detected by methods such as ethidium bromide staining of agarose gels, Southern or Northern blot hybridization, PCR or *in situ* hybridizations. Hybridization typically involves Southern or Northern blotting (see, for example, sections 9.37-9.52 of Sambrook et al., 1989, *"Molecular Cloning, A Laboratory Manual"*, 2nd Edition, Cold Spring Harbor Press, Plainview; NY). Probes should hybridize under high stringency conditions to a nucleic acid or the complement thereof. High stringency conditions can include the use of low ionic strength and high temperature washes, for example 0.015 M NaCl/0.0015 M sodium citrate (0.1X SSC), 0.1% sodium dodecyl sulfate (SDS) at 65°C. In addition, denaturing agents, such as formamide, can be employed during high stringency hybridization, e.g., 50% formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C.

Transgenic Plants

The invention provides a plant containing an exogenous nucleic acid that encodes a polypeptide of the invention, *e.g.*, nucleic acids encoding a polypeptide having an amino acid sequence as shown in SEQ ID NOS:8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 36.

Accordingly, a method according to the invention comprises introducing a nucleic acid construct into a plant cell and producing a plant (and progeny of such a plant) from the transformed cell. Techniques for introducing exogenous nucleic acids into monocotyledonous and dicotyledonous plants are known in the art, and include, without limitation, *Agrobacterium*-mediated transformation, viral vector-mediated transformation, electroporation and particle gun transformation, *e.g.*, U.S. Patents 5,204,253 and 6,013,863. If cell or tissue cultures are used as the recipient tissue for transformation, plants can be regenerated from transformed cultures by techniques known to those skilled in the art. Transgenic plants may be entered into a breeding program, *e.g.*, to introduce a nucleic acid encoding a polypeptide into other lines, to transfer the nucleic acid to other species or for further selection of other desirable traits. Alternatively, transgenic plants may be propagated vegetatively for those species amenable to such techniques. Progeny includes descendants of a particular plant or plant line. Progeny of an instant plant include seeds formed on F₁, F₂, F₃, and subsequent generation plants, or seeds formed on BC₁, BC₂, BC₃, and subsequent generation plants. Seeds produced by a transgenic plant can be grown and then selfed (or outcrossed and selfed) to obtain seeds homozygous for the nucleic acid encoding a novel polypeptide.

In another aspect, the invention provides a method of altering very long chain fatty acids in an organism. The method involves introducing an exogenous nucleic acid into the organism. The organism may be, for example, a yeast or a plant. A nucleic acid construct of the invention can alter the levels of very long chain fatty acids in plant tissues expressing the novel polypeptide, compared to VLCFA levels in corresponding tissues from a plant that does not contain or does not express the polypeptide. A comparison can be made, for example, between a transgenic plant of a plant line and a plant of the same line that lacks the nucleic acid construct or does not express the nucleic acid construct in

that tissue. Plants having an altered VLCFA composition may be identified by techniques known to the skilled artisan, *e.g.*, thin layer chromatographic or gas-liquid chromatographic (GLC) analysis of the appropriate plant tissue. Novel polypeptides can catalyze the conversion of oleic acid (18:1) to eicosenoic acid (20:1), and the conversion
5 of eicosenoic acid to erucic acid (22:1). In some embodiments, the ratio of erucic acid to eicosenoic acid (22:1/20:1) is greater than or equal to 0.20, as measured in the yeast microsome assay described below.

A suitable group of plants with which to practice the invention include dicots, such as alfalfa, soybean, rapeseed (high erucic and canola), safflower, or sunflower, and
10 monocots, such as corn, wheat, rye, barley, rice, or sorghum. Suitable rapeseed species include *B. napus*, *B. rapa*, *B. juncea*, and *B. hirta*. Additional plant species suitable for use in the present invention include *Sinapsis alba*, *Crambe abyssinica*, *Limnanthes douglasii* and *L. alba*.

Suitable tissues in which to express polynucleotides and/or polypeptides of the
15 invention include, without limitation, seeds, stems and leaves. Seeds expressing a novel coding sequence can be used to extract an oil having elevated levels of eicosenoic acid and/or erucic acid. Leaf tissues in which a novel coding sequence can be expressed include cells and tissues of the epidermis, *e.g.*, cells that are involved in forming trichomes. Also of interest are epidermal cells involved in forming the cuticular layer.
20 The cuticular layer comprises various very long chain fatty acids and VLCFA derivatives such as alkanes, esters, alcohols and aldehydes. Increasing the amount of VLCFAs in epidermal cells and tissues may enhance defense mechanisms and drought tolerance of plants.

The invention will be further described in the following examples, which do not
25 limit the scope of the invention described in the claims.

EXAMPLES

Example 1—Construction and Cloning of Nucleic Acids

Nucleic acids encoding chimeric polypeptides were generated by an overlap
30 polymerase chain reaction (PCR) strategy. Horton et al. (1989), *Gene*, 77:61-68 and see Figure 1 of Ho et al. (1989), *Gene*, 77:51-59. Briefly, a first round of PCR products were

generated in separate reactions using *Arabidopsis thaliana* FAE1 and *Brassica napus* elongase KCS nucleic acid as template. Nucleic acid sequences of the *A. thaliana* FAE1 and *B. napus* elongase KCS templates are shown in SEQ ID NO:1 and 3, respectively. The portion of each template that was amplified corresponded to the segment to be
5 combined in a desired chimera. The amino-terminal fragment of a given chimera was amplified using a 5' universal primer (sense) and a 3' chimera-specific primer (anti-sense). The carboxy-terminal fragment of a given chimera was amplified with a 5' chimera-specific primer (sense) and a 3' universal primer (anti-sense). Universal primer sequences are shown in Table 1 and SED ID NOS: 53-56. Chimera-specific primer
10 sequences are shown in Table 2 and SEQ ID NOS:43-52. The 5' and 3' universal primers anneal to the 5' and 3' ends of the template nucleic acid, respectively, and contain *Bam*HI and *Eco*RI restriction sites, respectively, for ease in subcloning into an expression vector. The 5' chimera-specific primers are antisense to the amino-terminal template and the 3' chimera-specific primers are antisense to the carboxy-terminal template. The 5' and 3'
15 chimera-specific primers each contain an internal complementary sequence where a switch occurs from the At to Bn sequence, or alternatively, from Bn to At.

The products produced by the first round of PCR were purified, and a second round of PCR was conducted using a mixture of the products from the first round of PCR as template nucleic acid. The appropriate 5' and 3' universal primers were used to
20 generate the chimeric nucleic acid product in the second round PCR. The amplified product was then digested with *Bam*HI and *Eco*RI, ligated into pYES2 (Invitrogen, Carlsbad, CA) and transformed into *E. coli*. pYES2 is a yeast centromere-containing, episomal plasmid that is stably propagated in both *E. coli* and in yeast. Each nucleic acid was inserted downstream of the GAL1 promoter in pYES2. The GAL1 promoter is
25 induced in yeast when galactose is present in the medium and repressed when glucose is present in the growth medium.

Nucleic acids encoding polypeptides with site-directed alterations in the coding sequence were also prepared by overlap PCR, using 5' and 3' chimera-specific primers in which the internal complementary region contained the desired sequence modification.

30

TABLE 1

Chimera type			
5' portio	3' portion	5' universal primer	3' universal primer
At	Bn	5'-ggggatccatgacgtccgtaacgtaagctcc-3' (SEQ ID NO:53)	5'-ccgaattottaggaccgaccgtttggacac-3' (SEQ ID NO:54)
Bn	At	5'-ggggatccatgacgtccattaacgtaagctcc-3' (SEQ ID NO:55)	5'-ccgaattottaggaccgaccgtttggacatgagtctt-3' (SEQ ID NO:56)

TABLE 2

Chimera	3' chimera-specific primers	5' chimera-specific primers
At173	5'-gcgctcgaaaatctattcaagaaca-3' (SEQ ID NO:43)	5'-gttctgaatagatttcgagcgaccgatgat-3' (SEQ ID NO:44)
At114	5'-cggaacggcacgtgtgatgattcgtct-3' (SEQ ID NO:45)	5'-aggacggatcatcacgcgcacgttcg-3' (SEQ ID NO:46)
At74	5'-cccaaaccggtttacctcgttga-3' (SEQ ID NO:47)	5'-tcaacgaggtaaaccggattggg-3' (SEQ ID NO:48)
At114 L91C K92R	5'-ccgcattgcagagttagtgtctctaaa-3' (SEQ ID NO:49)	5'-tttagagacactaactctgcaatgcgg-3' (SEQ ID NO:50)
At114 K92R	5'-ccaccgcattcagagttagtgtctct-3' (SEQ ID NO:51)	5'-agagacactaactctgagatcggtgg-3' (SEQ ID NO:52)

5 Due to a degeneracy in the primer used to generate the nucleic acids encoding carboxy-terminal sequences from *B. napus*, the amino acid residue at the fifth to last position from the carboxy-terminus in the polypeptides designated At114, At114 L91C K92R, At114 K92R and At254 is a P and the polypeptide designated At74 is a Q at that position as indicated in Fig. 1. The polypeptides designated At173 and At399 may have a

10 P or a Q at this position and are shown as Q in Fig. 1. A Q is found in the wild-type Bn polypeptide sequence at this position. In addition, due to PCR infidelity in the preparation of the nucleic acid encoding At114, the amino acid residue at position 439 of SEQ ID NO:8 may be an A or a T, with an A being found in the wild-type Bn sequence. In addition, PCR infidelity in the preparation of the nucleic acid encoding At114 L91C

15 K92R resulted in the residue at position 119 being an N. Position 119 in the wild-type Bn amino acid sequence is a D. Based on the data presented below, this residue can be either a D or an N without any apparent effect on activity.

Mutagenesis was confirmed by automated DNA sequencing, and each construct was used to transform *S. cerevisiae* strain InvScl (Invitrogen) using a lithium-acetate procedure (Gietz, R. and Woods, R., in *Molecular Genetics of Yeast: Practical Approaches*, Oxford Press, pp. 121-134 (1994)).

5

Example 2—Fatty Acid Elongase KCS Activity in Yeast Microsomes

Elongase KCS enzymatic activity was analyzed by preparing microsomes from transformed yeast cells and assaying these microsomes *in vitro* for elongase KCS activity. Transformed yeast cells were grown overnight in YPD media at 30°C with vigorous shaking. Complete minimal uracil dropout media (cm-ura) supplemented with galactose (2% weight/volume in 40 ml) was inoculated to an OD₆₀₀ of 0.002 to 0.01. Cultures were grown at 30°C to an OD₆₀₀ of approximately 1.5 to 2.0. Cells were harvested by centrifugation at 5000 xg for 10 min and washed with 10 ml ice cold isolation buffer (IB), which contains 80 mM Hepes-KOH (pH 7.2), 5 mM EGTA, 5 mM EDTA, 10 mM KCl, 320 mM sucrose and 2 mM DTT). Cells were then resuspended in enough IB to fill a 1.7 ml tube containing 700 µl of 0.5 µm glass beads and yeast microsomes were isolated from the cells essentially as described in Tillman, T. & Bell, R., *J. Biol. Chem.* 261:9144-9149 (1986). The microsomal membrane pellet was recovered by centrifugation at 252,000 xg for 60 min. Microsomal pellets were resuspended in a minimal volume of IB, and the protein concentration adjusted to 2.5 µg µl⁻¹ by addition of IB containing 15% glycerol. Microsomes were frozen on dry ice and stored at -80°C. The protein concentration in microsomes was determined by the Bradford method (Bradford, *Anal. Biochem.*, 72:248-54, 1976).

Elongase KCS activity was measured essentially as described in Hlousek-Radojcic, et al., *Plant J.* 8:803-809 (1995). Briefly, the standard elongation reaction mix contained 80 mM Hepes-KOH (pH 7.2), 20 mM MgCl₂, 500 µM NADPH, 100 µM malonyl-CoA, 10 µM CoA-SH and 15 µM [¹⁴C]18:1-CoA (50 µCi µmol⁻¹). The reaction was initiated by the addition of yeast microsomes (6 µg protein) and the mixture was incubated at 30°C, in a final reaction volume of 25 µl. Reaction time was 10 min unless indicated otherwise.

30

Methyl esters of the acyl-CoA elongase products were prepared by incubation with 500 μ l 2% H₂SO₄/MeOH at 80°C for 2 h. Extracted methyl esters were separated on reverse phase silica gel TLC plates (Analtech, Newark, DE), quantified by phosphorimaging, and analyzed by ImageQuant software (Molecular Dynamics, Inc., Sunnyvale, CA). The detection limit for each product is about 0.001 nmoles/min/mg microsomal protein, depending on the phosphorimage exposure time.

Example 3—Elongase KCS Substrate Specificity

Table 3 is a summary of elongase activity and product ratios of *B. napus* (Bn) and *A. thaliana* (At) elongase KCS nucleic acid sequences expressed in yeast and assayed as described in Example 2. Microsomes prepared from galactose-induced yeast expressing the indicated nucleic acid were assayed after 10 min for conversion of labeled oleoyl substrate to eicosenoyl product, erucyl product, and lignoceryl product. For convenience, fatty acyl substrates and products are oftentimes referred to as the acid rather than as the acyl or acyl CoA. The ratio of 22:1 product to 20:1 product is also shown. Experiments were performed on 17 individual yeast transformants for each construct.

TABLE 3¹

	18:1(\pm sd)	20:1(\pm sd)	22:1(\pm sd)	20:1+22:1(\pm sd)	22:1/20:1(\pm sd)
<i>B. napus</i> elongase KCS (SEQ ID NO:4)	45 \pm 4	3.3 \pm 0.4	1.4 \pm 0.5	4.8 \pm 0.2	0.43 \pm 0.11
<i>A. thaliana</i> FAE1 (SEQ ID NO:2)	29 \pm 9	6 \pm 0.8	1.2 \pm 0.2	7.1 \pm 0.9	0.20 \pm 0.04

¹Amounts of oleic acid (18:1), eicosenoic acid (20:1), erucic acid (22:1), and the sum of 20:1 and 22:1, are expressed as nmol/mg microsomal protein; \pm sd = standard deviation.

Table 4 shows the ratio of 22:1/20:1 products produced by Bn, At, and various chimeric polypeptides after incubation of the microsomes with the labeled 18:1 substrate for 5, 10 or 20 min. The results shown in Table 4 represent 4 different microsome preparations from a single yeast transformant with each construct and 2-3 assays of each microsomal preparation. The At FAE1 (SEQ ID NO:2) produces about 5 times more eicosenoic acid than erucic acid. In contrast, the Bn elongase KCS (SEQ ID NO:4) produces about 2-3 times more eicosenoic acid than erucic acid. See also Table 3.

The At254, At173 and At114 polypeptides have a 22:1/20:1 product ratio that is similar to that of wild-type At *FAEI*, whereas the At74 polypeptide has a product ratio that is similar to that of wild-type Bn (Table 4). These results indicate that amino acids affecting product specificity are present between residues 75 and 114 of the wild-type At
 5 elongase KCS. The At74 gene product possesses the amino acid sequence of the Bn elongase KCS of SEQ ID NO:4 at positions 75 to 114, indicating that amino acids of the Bn elongase KCS that differ from the at *FAEI* in this region contribute to the difference in C22:1/C20:1 product ratio.

10

TABLE 4

Time (min)	Polypeptide Assayed ¹						
	Bn (SEQ ID NO:4)	At (SEQ ID NO:2)	At254 (SEQ ID NO:24)	At173 (SEQ ID NO:26)	At114 (SEQ ID NO:8)	At74 (SEQ ID NO:10)	At114 L91C K92R (SEQ ID NO:12)
5	0.35±0.07	0.18±0.04	0.14±0.03	0.11±0.07	0.17±0.04	0.42±0.07	0.22±0.02
10	0.33±0.10	0.13±0.01	0.11±0.03	0.08±0.01	0.15±0.03	0.36±0.06	0.20±0.02
20	0.35±0.13	0.13±0.02	0.12±0.03	0.11±0.05	0.16±0.04	0.29±0.05	0.20±0.04

¹ The data are the C22:1/C20:1 ratio ± standard deviation

Site-directed modifications were made to the At114 or At74 nucleic acid sequence within the region corresponding to residues 75 to 114 in order to determine which amino
 15 acids contributed to the altered product ratio. The modified nucleic acids were made according to the overlap PCR strategy described in Example 1 and the constructs were introduced into yeast. Elongase KCS activity was measured as described in Example 2. The results showed that changing the At114 amino acid sequence from alanine to serine and glutamine to lysine at positions 157 and 163, respectively, resulted in undetectable
 20 elongase activity. Likewise, changing serine and isoleucine at positions 93 and 95 within At74 to valine in both positions also resulted in undetectable elongase activity.

However, when the leucine and lysine residues at positions 91 and 92 within the At114 polypeptide were changed to cysteine and arginine, respectively, the C22:1/C20:1 product ratio of the resulting polypeptide, At114 L91C K92R, was shifted to more closely
 25 resemble that of the wild-type Bn polypeptide (Table 4).

Site-directed modifications were made to the At114 nucleic acid sequence to generate coding sequences for two new polypeptides, one bearing the leucine to cysteine modification and one bearing the lysine to arginine modification. These polypeptides were designated At114 L91C and At114 K92R. The nucleotide sequence of the nucleic acid encoding At114 K92R is shown in SEQ ID NO:13 and the amino acid sequence of the polypeptide is shown in SEQ ID NO:14. The two nucleic acids were introduced into yeast and the activity of each polypeptide was analyzed in yeast microsomal assays. The results showed that the L to C-modified polypeptide, At114 L91C, had low but detectable catalytic activity. The K to R-modified polypeptide, At114 K92R, had a higher 22:1/20:1 ratio that approached that of wild-type Bn (Table 5). Results presented are the mean of 1 to 3 individual assays each of at least 7 separate microsomal preparations.

TABLE 5

	20:1+22:1 ¹	(22:1/20:1)
At (SEQ ID NO:2)	16.0 +/- 2.7	0.15 +/- 0.04
Bn (SEQ ID NO:4)	9.8 +/- 3.2	0.32 +/- 0.07
At114 K92R (SEQ ID NO:14)	5.8 +/- 3.1	0.32 +/- 0.09

¹ The sum of the amounts of eicosenoic acid (20:1) and erucic acid (22:1) is expressed as nmole/mg microsomal protein.

Example 4—Elongase KCS Catalytic Activity

Table 6 shows the results of yeast microsomal assays of Bn elongase KCS, At *FAE1*, and various chimeric polypeptides for various incubation times. The data in Table 6 show the sum of C20:1 and C22:1 in nmole/mg protein from microsomal preparations assayed 2 to 3 times each.

The results indicate that the amount of elongase KCS activity of the wild-type At *FAE1* is about 1.5 to 2 times higher than that of wild-type Bn elongase KCS. The At114 polypeptide has an activity that is intermediate between the wild-type At and wild-type Bn, while the At74 polypeptide has an activity that is lower than that of wild-type Bn enzymes. These results indicate that modifying amino acid residues in the region from position 74 to 114 affects elongase activity.

The activity of the At114 L91C K92R gene product was measured in yeast microsomes and is shown in Table 6. The elongase activity of this polypeptide was higher than that of At114.

5

TABLE 6¹

Time (min)	pYES2	Bn (SEQ ID NO:2)	At (SEQ ID NO:4)	At114 (SEQ ID NO:8)	At74 (SEQ ID NO:10)	At114 L91C K92R (SEQ ID NO:12)
0	-2.4±2.4	2.7±1.8	2.4±1.8	1.4±1.0	2.2±0.84	2.3±1.08
5	0.24±0.6	5.1±1.6	8.7±1.2	5.9±0.6	3.2±1.1	6.5±1.0
10	0.78±0.6	7.4±1.8	12.1±0.6	8.8±0.5	4.1±0.8	9.6±1.2
20	0.96±0.6	7.8±2.1	13.7±1.8	10.1±1.2	4.4±0.8	11.5±1.1
45	1.32±0.6	8.1±2.2	14.0±0.6	10.2±1.2	4.6±0.5	12.1±0.9

¹ The data are the sum of the C20:1 and C22:1 elongase products (nmole/mg microsomal protein) ± standard deviation.

The elongase activity of the At114 L91C and At114 K92R polypeptides were also assayed in yeast microsomes. The results indicated that the catalytic activity of the At114 L91C polypeptide was about 15-30% of the activity of At114, whereas the activity of At114 K92R was approximately the same as that of At114.

A yeast microsome assay was carried out to compare the Bn elongase KCS shown in SEQ ID NO:4 and another naturally-occurring elongase KCS from the *B. napus* cultivar Askari. The elongase KCS from Askari has the same sequence as that shown in SEQ ID NO:4, except for a valine at position 4 and an aspartic acid at position 307. The results indicated that the Askari elongase KCS had a higher elongase activity and a higher C22:1/C20:1 ratio than did the Bn elongase KCS of SEQ ID NO:4.

Site-directed modifications to SEQ ID NO:3 were made by the techniques described in Example 2 to generate nucleic acids encoding polypeptides Bn I4V, Bn G307D and Bn I4V G307D. The latter polypeptide has the same amino acid sequence as the naturally occurring Askari elongase KCS. After cloning and transforming of each construct into yeast as described in Example 2, microsome assays were performed. Table 7 presents the results from a single experiment in which elongase activity and product ratios for the elongase KCS constructs were measured. Assays were performed as

described in Example 2. The results indicate that changing the residue at position 4 from isoleucine to valine had little or no effect on the elongase activity or the C22:1/C20:1 ratio. On the other hand, the Bn G307D polypeptide had a higher elongase activity and produced more C22:1 product than did the unmodified wild-type Bn polypeptide. The amino acid sequence of Bn G307D is shown in SEQ ID NO:34.

TABLE 7¹

	18:1	20:1	22:1	24:1	22:1/20:1	20:1+22:1
Bn	47.9	5.5	1.9	0.3	0.35	7.7
Bn I4V	48.4	5.5	2.0	0.4	0.37	7.8
Bn G307D	37.2	6.7	5.4	0.7	0.80	12.7
Bn I4V G307D	41.9	6.5	4.5	0.5	0.68	11.6
<i>B. napus</i> (Ask)	37.6	7.7	6.7	0.8	0.86	15.2

¹ Amounts of oleic acid (18:1), eicosenoic acid (20:1), erucic acid (22:1), lignoceric acid (24:1), and the sum of 20:1 and 22:1, are expressed as nmol/mg microsomal protein.

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It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

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 His Leu Tyr Tyr Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro
 45 50 55

ctc ttg gcc ttc acc gtt ttc ggt tcg gtt ctc tac atc gca acc cgg 303
 Leu Leu Ala Phe Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg
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ccc aaa ccg gtt tac ctc gtg gag tac tca tgc tac ctt cca cca acg 351
 Pro Lys Pro Val Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr
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 His Cys Arg Ser Ser Ile Ser Lys Val Met Asp Ile Phe Phe Gln Val
 90 95 100 105

aga aaa gct gat cct tct cgg aac ggc acg tgc gat gac tcg tcc tgg 447
 Arg Lys Ala Asp Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp
 110 115 120

ctt gac ttc ttg agg aag att caa gaa cgt tca ggt cta ggc gat gaa 495
 Leu Asp Phe Leu Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu
 125 130 135

acc cac ggg ccc gag ggg ctg ctt cag gtc cct ccc cgg aag act ttt 543

WO 01/94565

PCT/US01/18737

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Ala	Arg	Ala	Arg	Glu	Glu	Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	
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aat	cta	ttc	aag	aac	acc	aat	gtt	aac	cct	aaa	gat	ata	ggc	ata	ctt	639
Asn	Leu	Phe	Lys	Asn	Thr	Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	
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Val	Val	Asn	Ser	Ser	Met	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	
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gtc	gtt	aac	act	ttc	aag	ctc	cga	agc	aac	gta	aga	agc	ttt	aac	ctt	735
Val	Val	Asn	Thr	Phe	Lys	Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	
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ggc	ggc	atg	ggc	tgt	agt	gcc	ggc	gtt	ata	gcc	att	gat	cta	gca	aag	783
Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	
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gac	ttg	ttg	cat	gtc	cat	aaa	aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	831
Asp	Leu	Leu	His	Val	His	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	
	235					240					245					
gag	aac	atc	act	tat	aac	att	tac	gct	ggc	gat	aat	agg	tcc	atg	atg	879
Glu	Asn	Ile	Thr	Tyr	Asn	Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	
250					255					260					265	
gtt	tca	aat	tgc	ttg	ttc	cgt	gtt	ggc	ggg	gcc	gct	att	ttg	ctc	tcc	927
Val	Ser	Asn	Cys	Leu	Phe	Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	
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Asn	Lys	Pro	Arg	Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	
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Val	Arg	Thr	His	Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	
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Gln	Gly	Asp	Asp	Glu	Asn	Gly	Gln	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	
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Ile	Thr	Asp	Val	Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	
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ggc	ccg	ttg	att	ctt	ccg	tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	1167
Gly	Pro	Leu	Ile	Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	
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Phe	Met	Gly	Lys	Lys	Leu	Phe	Lys	Asp	Glu	Ile	Lys	His	Tyr	Tyr	Val	
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ccg	gac	ttc	aag	ctt	gct	atc	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	1263
Pro	Asp	Phe	Lys	Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	

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aaa gcc gtg att gat gtg cta gag aag aac cta ggc cta gca ccg atc			1311
Lys Ala Val Ile Asp Val Leu Glu Lys Asn Leu Gly Leu Ala Pro Ile			
395	400	405	
gat gta gag gca tca aga tca acg tta cat aga ttt gga aac act tca			1359
Asp Val Glu Ala Ser Arg Ser Thr Leu His Arg Phe Gly Asn Thr Ser			
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tct agc tca ata tgg tat gag ttg gca tac ata gaa ccc aaa gga agg			1407
Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Ile Glu Pro Lys Gly Arg			
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Lys Cys Asn Ser Ala Val Trp Val Ala Leu Asn Asn Val Lys Ala Ser			
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Thr Asn Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys Ile			
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Asp Ser Asp Ser Gly Lys Ser Glu Thr Arg Val Pro Asn Gly Arg Ser			
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Ala Tyr Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr Leu			
	35	40	45
Gln His Asn Leu Ile Thr Ile Ala Pro Leu Leu Ala Phe Thr Val Phe			
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Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu Val			
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Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser			
	85	90	95
Lys Val Met Asp Ile Phe Phe Gln Val Arg Lys Ala Asp Pro Ser Arg			
	100	105	110
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile			
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Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu			
	130	135	140
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Arg Ala Arg Glu Glu Thr			
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Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn			

48

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Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
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ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
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Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
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Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
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Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
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Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
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Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
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Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
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Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
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Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
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Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
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Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
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Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
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Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
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Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
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Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
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Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
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Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
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Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
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Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
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cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
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Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys	
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Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
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Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35 40 45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50 55 60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65 70 75 80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
85 90 95
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
100 105 110
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
115 120 125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
130 135 140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
145 150 155 160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
165 170 175
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
180 185 190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195 200 205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210 215 220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225 230 235 240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
245 250 255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
260 265 270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
275 280 285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
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Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305 310 315 320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
325 330 335

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Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
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Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
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Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
      385      390      395      400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
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Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
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Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys
      435      440      445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
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Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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 3' 1296 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At74

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Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
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Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
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Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
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Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile	
115 120 125	
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Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu	
130 135 140	
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Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr	
145 150 155 160	
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Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn	
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Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe	
180 185 190	
aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag ctc	624
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu	
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225 230 235 240	
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Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg	
260 265 270	
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Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg	
275 280 285	
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Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala	
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Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg	
325 330 335	
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      355                      360                      365

aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct att      1152
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
      370                      375                      380

gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg cta      1200
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
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Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
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acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat gag      1296
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
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Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
      435                      440                      445

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<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 74 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 431 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At74

<400> 10

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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1           5           10           15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
      20           25           30
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
      35           40           45

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Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80
 Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg
 100 105 110
 Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile
 115 120 125
 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu
 130 135 140
 Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr
 145 150 155 160
 Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn
 165 170 175
 Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
 180 185 190
 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
 195 200 205
 Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
 210 215 220
 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
 225 230 235 240
 Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
 245 250 255
 Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
 260 265 270
 Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
 275 280 285
 Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala
 290 295 300
 Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly
 305 310 315 320
 Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg
 325 330 335
 Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
 340 345 350
 Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
 355 360 365
 Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
 370 375 380
 Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
 385 390 395 400
 Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
 405 410 415
 Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
 420 425 430
 Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
 435 440 445
 Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
 450 455 460
 Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
 465 470 475 480
 Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
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 Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 11

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and
 3' 1179 bp from *B. napus* elongase KCS (SEQ ID
 NO:3) having mutations at positions 271, 272 and
 275; designated At114 L91C K92R

<221> CDS

<222> (1)...(1518)

<400> 11

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat tgc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat aat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	

ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344

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Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc cca aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 12

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 392 amino acids from B. napus
 elongase KCS (SEQ ID NO:4) having mutations at
 residues 91 and 92; designated At114 L91C K92R

<400> 12

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
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Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80

Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser
 85 90 95

Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110

Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125

Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140

Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160

Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175

Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190

Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205

Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His

225		230		235		240
Lys Asn Thr Tyr	Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn					
	245		250		255	
Ile Tyr Ala Gly	Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe					
	260		265		270	
Arg Val Gly Gly	Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg					
	275		280		285	
Arg Arg Ser Lys Tyr	Glu Leu Val His Thr Val Arg Thr His Thr Gly					
	290		295		300	
Ala Asp Gly Lys Ser	Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn					
305	310		315		320	
Gly Lys Ile Gly	Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly					
	325		330		335	
Arg Thr Val Lys	Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro					
	340		345		350	
Leu Ser Glu Lys	Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu					
	355		360		365	
Phe Lys Asp Lys	Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala					
370	375		380			
Ile Asp His Phe	Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val					
385	390		395		400	
Leu Glu Lys Asn	Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg					
	405		410		415	
Ser Thr Leu His	Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr					
	420		425		430	
Glu Leu Ala Tyr	Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys					
	435		440		445	
Val Trp Gln Ile	Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val					
	450		455		460	
Trp Val Ala Leu	Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu					
465	470		475		480	
His Cys Ile Asp	Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys					
	485		490		495	
Ser Glu Thr Arg	Val Pro Asn Gly Arg Ser					
	500		505			

<210> 13

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3), having a mutation at position 275;
 designated At114 K92R

<221> CDS

<222> (1)...(1518)

<400> 13

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	

35	40	45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc			192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe			
50	55	60	
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt			240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val			
65	70	75	80
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct			288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser			
	85	90	95
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca			336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser			
	100	105	110
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag			384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys			
	115	120	125
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg			432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly			
	130	135	140
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag			480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu			
145	150	155	160
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc			528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr			
	165	170	175
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg			576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
	180	185	190
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag			624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
	195	200	205
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt			672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
	210	215	220
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat			720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac			768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
	245	250	255
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc			816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
	260	265	270
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt			864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
	275	280	285

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aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga      912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
290                               295                               300

gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac      960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305                               310                               315                               320

ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt      1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
325                               330                               335

cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg      1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
340                               345                               350

tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt      1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
355                               360                               365

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct      1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
370                               375                               380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg      1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385                               390                               395                               400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga      1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
405                               410                               415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat      1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
420                               425                               430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa      1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
435                               440                               445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt      1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450                               455                               460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa      1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465                               470                               475                               480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
485                               490                               495

tca gag act cgt gtc cca aac ggt cgg tcc taa      1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
500                               505

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<210> 14
 <211> 506
 <212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4), having a mutation at position 92; designated At114 K92R

<400> 14

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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
		20						25					30		
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
		50				55					60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65					70					75				80	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser
				85					90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
		130				135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145					150					155					160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165						170					175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180					185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195					200					205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
		210				215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235					240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245						250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
		260					265						270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
		275					280						285		
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
		290				295					300				
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305					310					315					320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325						330					335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
		340						345					350		
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu
		355				360					365				
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
		370				375					380				
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val
385					390					395					400
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg
			405						410					415	


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Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420      425      430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435      440      445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450      455      460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
      465      470      475      480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
      485      490      495
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
      500      505

```

<210> 15

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from *A. thaliana* FAEl (SEQ ID NO:1) and
 3' 1179 bp from *B. napus* elongase KCS (SEQ ID
 NO:3), having a mutation at position 920;
 designated At114 G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 15

```

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1              5              10              15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
      20              25              30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
      35              40              45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
      50              55              60

ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt      240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
      65              70              75              80

gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct      288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
      85              90              95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca      336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
      100             105             110

cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag      384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
      115             120             125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg      432

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Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly		
130						135					140						
ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	480	
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu		
145					150				155					160			
acg	gag	caa	gtt	atc	att	ggg	gcg	cta	gaa	aat	cta	ttc	aag	aac	acc	528	
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr		
				165					170					175			
aac	gtt	aac	cct	aaa	gat	ata	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	576	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met		
			180					185					190				
ttt	aat	cca	act	cca	tcg	ctc	tcc	gcg	atg	gtc	gtt	aac	act	ttc	aag	624	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys		
		195					200					205					
ctc	cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggg	ggc	atg	ggg	tgt	agt	672	
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser		
	210					215					220						
gcc	ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	720	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His		
225					230				235					240			
aaa	aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	768	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn		
				245					250					255			
att	tac	gct	ggg	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	816	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe		
			260					265					270				
cgt	gtt	ggg	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	864	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg		
		275					280					285					
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	912	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly		
		290				295					300						
gct	gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	960	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn		
305					310				315					320			
ggc	aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggg	1008	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly		
				325					330				335				
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggg	ccg	ttg	att	ctt	ccg	1056	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro		
			340					345					350				
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104	
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu		
		355					360					365					
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	1152	
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala		

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370	375	380	
att gac cat ttt tgt	ata cat gcc gga ggc	aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys	Ile His Ala Gly Gly	Arg Ala Val Ile Asp Val	
385	390	395 400	
cta gag aag aac cta	gcc cta gca ccg atc	gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu	Ala Leu Ala Pro Ile	Asp Val Glu Ala Ser Arg	
	405	410 415	
tca acg tta cat aga	ttt gga aac act tca	tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg	Phe Gly Asn Thr Ser	Ser Ser Ser Ile Trp Tyr	
	420	425 430	
gag ttg gca tac ata	gaa gca aaa gga agg	atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile	Glu Ala Lys Gly Arg	Met Lys Lys Gly Asn Lys	
	435	440 445	
gtt tgg cag att gct	tta ggg tca ggc ttt	aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala	Leu Gly Ser Gly Phe	Lys Cys Asn Ser Ala Val	
	450	455 460	
tgg gtg gct cta aac	aat gtc aaa gct tcg	aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn	Asn Val Lys Ala Ser	Thr Asn Ser Pro Trp Glu	
	465	470 475 480	
cac tgc atc gac aga	tac ccg gtc aaa att	gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg	Tyr Pro Val Lys Ile	Asp Ser Asp Ser Gly Lys	
	485	490 495	
tca gag act cgt gtc	caa aac ggt cgg tcc	taa	1521
Ser Glu Thr Arg Val	Gln Asn Gly Arg Ser		
	500	505	

<210> 16

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having mutation at residue 307; designated At114 G307D; hypothetical

<400> 16

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	

Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
	115						120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145				150					155					160	
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165					170						175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
	180							185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195						200					205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215				220					
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235				240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245					250						255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
	260							265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
	275						280					285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290					295					300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305					310					315				320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325					330						335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
		340						345					350		
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu
	355					360						365			
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
	370					375					380				
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val
385					390					395				400	
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg
			405					410						415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr
		420						425					430		
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys
	435						440					445			
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val
	450					455					460				
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu
465					470					475				480	
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys
			485					490						495	
Ser	Glu	Thr	Arg	Val	Gln	Asn	Gly	Arg	Ser						
		500						505							

<210> 17

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1296 bp from B. napus elongase KCS (SEQ ID
 NO:3) having a mutation at position 917;
 designated At74 G306D; hypothetical

<221> CDS

<222> (1)...(1515)

<400> 17

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aaa ccg gtt tac ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val	
65 70 75 80	
gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc tcc	288
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser	
85 90 95	
aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct cgg	336
Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg	
100 105 110	
aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag att	384
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile	
115 120 125	
caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg ctg	432
Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu	
130 135 140	
ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag acg	480
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr	
145 150 155 160	
gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc aac	528
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn	
165 170 175	
gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg ttt	576
Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe	
180 185 190	
aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag ctc	624
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu	
195 200 205	
cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt gcc	672
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala	
210 215 220	

ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat aaa	720
Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys	
225 230 235 240	
aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac att	768
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile	
245 250 255	
tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc cgt	816
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg	
260 265 270	
gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt aga	864
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg	
275 280 285	
cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga gct	912
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala	
290 295 300	
gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac ggc	960
Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly	
305 310 315 320	
aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt cga	1008
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg	
325 330 335	
acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg tta	1056
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu	
340 345 350	
agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt ttc	1104
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe	
355 360 365	
aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct att	1152
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile	
370 375 380	
gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg cta	1200
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu	
385 390 395 400	
gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga tca	1248
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser	
405 410 415	
acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat gag	1296
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu	
420 425 430	
ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa gtt	1344
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val	
435 440 445	
tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt tgg	1392
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp	
450 455 460	
gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa cac	1440

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Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
 465 470 475 480

tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag tca 1488
 Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
 485 490 495

gag act cgt gtc caa aac ggt cgg tcc taa 1518
 Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 18

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 74 amino acids from A. thaliana FAEL (SEQ ID
 NO:2) and 3' 431 amino acids from B. napus
 elongase KCS (SEQ ID NO:4) having a mutation at
 residue 306; designated At74 G306D; hypothetical

<400> 18

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80

Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
 85 90 95

Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg
 100 105 110

Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile
 115 120 125

Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu
 130 135 140

Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu Thr
 145 150 155 160

Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn
 165 170 175

Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
 180 185 190

Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
 195 200 205

Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
 210 215 220

Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
 225 230 235 240

Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
 245 250 255

Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
 260 265 270

Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
 275 280 285

Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala

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      290              295              300
Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly
305              310              315              320
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg
              325              330              335
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
              340              345              350
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
              355              360              365
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
              370              375              380
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
385              390              395              400
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
              405              410              415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
              420              425              430
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
              435              440              445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
              450              455              460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
465              470              475              480
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
              485              490              495
Glu Thr Arg Val Gln Asn Gly Arg Ser
              500              505

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<210> 19

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAEL (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3) having mutations at positions 271, 272, 275
 and 920; designated At114 L91C K92R G307D;
 hypothetical

<221> CDS

<222> (1)...(1518)

<400> 19

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1              5              10              15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
              20              25              30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
              35              40              45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
              50              55              60

ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt      240

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Gly 65	Leu	Val	Leu	Tyr	Ile 70	Val	Thr	Arg	Pro	Asn 75	Pro	Val	Tyr	Leu	Val 80	
gac	tac	tcg	tgt	tac	ctt	cgg	cca	cgg	cat	tgc	aga	gtt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Cys	Arg	Val	Ser	Val	Ser	
				85					90					95		
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
			100					105					110			
cgg	aac	ggc	acg	tgt	gat	aat	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	384
Arg	Asn	Gly	Thr	Cys	Asp	Asn	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				
att	caa	gaa	cgt	tca	ggc	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	
	130					135					140					
ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	480
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	
145					150					155					160	
acg	gag	caa	gtt	atc	att	ggc	gag	cta	gaa	aat	cta	ttc	aag	aac	acc	528
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
				165				170					175			
aac	gtt	aac	cct	aaa	gat	ata	ggc	ata	ctt	gtg	gtg	aac	tca	agc	atg	576
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180					185					190			
ttt	aat	cca	act	cca	tcg	ctc	tcc	gcg	atg	gtc	gtt	aac	act	ttc	aag	624
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
	195						200					205				
ctc	cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggc	ggc	atg	ggc	tgt	agt	672
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210					215					220					
gcc	ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	720
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
225					230					235				240		
aaa	aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	768
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	
				245					250					255		
att	tac	gct	ggc	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	816
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
			260				265						270			
cgt	gtt	ggc	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	864
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
		275					280					285				
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	912
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	
		290				295					300					
gct	gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	960
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	

WO 01/94565

PCT/US01/18737

305	310	315	320	
ggc aaa atc gga	gtg agt ttg tcc aag	gac ata acc gat	gtt gct ggt	1008
Gly Lys Ile Gly	Val Ser Leu Ser Lys	Asp Ile Thr Asp	Val Ala Gly	
	325	330	335	
cga acg gtt aag	aaa aac ata gca	acg ttg ggt ccg	ttg att ctt ccg	1056
Arg Thr Val Lys	Lys Asn Ile Ala Thr	Leu Gly Pro Leu	Ile Leu Pro	
	340	345	350	
tta agc gag aaa	ctt ctt ttt ttc	gtt acc ttc atg	ggc aag aaa ctt	1104
Leu Ser Glu Lys	Leu Leu Phe Phe	Val Thr Phe Met	Gly Lys Lys Leu	
	355	360	365	
ttc aaa gat aaa	atc aaa cat tac	tac gtc ccg gat	ttc aaa ctt gct	1152
Phe Lys Asp Lys	Ile Lys His Tyr	Tyr Val Pro Asp	Phe Lys Leu Ala	
	370	375	380	
att gac cat ttt	tgt ata cat gcc	gga ggc aga gcc	gtg att gat gtg	1200
Ile Asp His Phe	Cys Ile His Ala	Gly Gly Arg Ala	Val Ile Asp Val	
	385	390	395	400
cta gag aag aac	cta gcc cta gca	ccg atc gat gta	gag gca tca aga	1248
Leu Glu Lys Asn	Leu Ala Leu Ala	Pro Ile Asp Val	Glu Ala Ser Arg	
	405	410	415	
tca acg tta cat	aga ttt gga aac	act tca tct agc	tca ata tgg tat	1296
Ser Thr Leu His	Arg Phe Gly Asn	Thr Ser Ser Ser	Ser Ile Trp Tyr	
	420	425	430	
gag ttg gca tac	ata gaa gca aaa	gga agg atg aag	aaa ggt aat aaa	1344
Glu Leu Ala Tyr	Ile Glu Ala Lys	Gly Arg Met Lys	Lys Lys Gly Asn	Lys
	435	440	445	
gtt tgg cag att	gct tta ggg tca	ggc ttt aag tgt	aac agt gca gtt	1392
Val Trp Gln Ile	Ala Leu Gly Ser	Gly Phe Lys Cys	Asn Ser Ala Val	
	450	455	460	
tgg gtg gct cta	aac aat gtc aaa	gct tcg aca aat	agt cct tgg gaa	1440
Trp Val Ala Leu	Asn Asn Val Lys	Ala Ser Thr Asn	Ser Pro Trp Glu	
	465	470	475	480
cac tgc atc gac	aga tac ccg gtc	aaa att gat tct	gat tca ggt aag	1488
His Cys Ile Asp	Arg Tyr Pro Val	Lys Ile Asp Ser	Asp Ser Gly Lys	
	485	490	495	
tca gag act cgt	gtc caa aac ggt	cgg tcc taa		1521
Ser Glu Thr Arg	Val Gln Asn Gly	Arg Ser		
	500	505		

<210> 20

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutations at positions 91, 92 and 307; designated At114 L91C

K92R G307D; hypothetical

<400> 20

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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1           5           10           15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
          20           25           30
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
          35           40           45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
          50           55           60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65           70           75           80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser
          85           90           95
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
          100          105          110
Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys
          115          120          125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
          130          135          140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
145          150          155          160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
          165          170          175
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
          180          185          190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
          195          200          205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
          210          215          220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225          230          235          240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
          245          250          255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
          260          265          270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
          275          280          285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
          290          295          300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305          310          315          320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
          325          330          335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
          340          345          350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
          355          360          365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
          370          375          380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385          390          395          400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
          405          410          415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
          420          425          430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
          435          440          445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
          450          455          460

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Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 21

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAEL (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3) having mutations at positions 275 and 920;
 designated At114 K92R G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 21

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 175	528
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	576
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 255	768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370 375 380	1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385 390 395 400	1200

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cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga      1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
              405                      410                      415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat      1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
              420                      425                      430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa      1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
              435                      440                      445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt      1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
              450                      455                      460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa      1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465              470              475              480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
              485              490              495

tca gag act cgt gtc caa aac ggt cgg tcc taa      1521
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
              500              505

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<210> 22

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutations at positions 92 and 307; designated At114 K92R G307D; hypothetical

<400> 22

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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
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Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
              20              25              30
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
              35              40              45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
              50              55              60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65              70              75              80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser
              85              90              95
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
              100              105              110
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
              115              120              125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
              130              135              140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu

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145          150          155          160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
          165          170          175
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
          180          185          190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
          195          200          205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
          210          215          220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225          230          235          240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
          245          250          255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
          260          265          270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
          275          280          285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
          290          295          300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305          310          315          320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
          325          330          335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
          340          345          350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
          355          360          365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
          370          375          380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385          390          395          400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
          405          410          415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
          420          425          430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
          435          440          445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
          450          455          460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465          470          475          480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
          485          490          495
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
          500          505

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<210> 23

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 762 bp from A. thaliana FAEL (SEQ ID NO:1) and
 3' 759 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At254

<221> CDS

<222> (1)...(1518)

<400> 23

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac

48

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	
1				5					10					15		
ttt	ttc	aac	ctc	tgt	ttg	ttc	cgc	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
		20					25					30				
gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ctc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Leu	Leu	Ser	Tyr	Leu	
		35					40				45					
caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	gtt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
	50					55				60						
ggc	ttg	gtt	ctc	tac	atc	gta	acc	cga	ccc	aat	cgc	gtt	tat	ctc	gtt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
65					70				75					80		
gac	tac	tgc	tgt	tac	ctt	cca	cca	cgc	cat	ctc	aaa	gtt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	
			85					90						95		
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
			100				105						110			
cgc	aac	gtg	gca	tgt	gat	gat	cgc	tcc	tgc	ctc	gat	ttc	ctg	agg	aag	384
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	
	115						120					125				
att	caa	gag	cgt	tca	ggc	cta	ggc	gat	gag	acg	tac	agt	cct	gag	gga	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	
	130				135						140					
ctc	att	cac	gta	cca	cgc	cgc	aag	act	ttt	gca	gcg	tca	cgt	gaa	gag	480
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	
145					150					155				160		
aca	gag	aag	gtt	atc	atc	ggc	gcg	ctc	gaa	aat	cta	ttc	gag	aac	acc	528
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr	
			165					170					175			
aaa	gtt	aac	cct	aga	gag	att	ggc	ata	ctt	gtg	gtg	aac	tca	agc	atg	576
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
		180					185						190			
ttt	aat	cca	act	cct	tgc	cta	tcc	gct	atg	gtc	gtt	aat	act	ttc	aag	624
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
	195					200						205				
ctc	cga	agc	aac	atc	aaa	agc	ttt	aat	cta	gga	gga	atg	ggc	tgt	agt	672
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210				215					220						
gct	ggc	gtt	att	gcc	att	gat	ttg	gct	aaa	gac	ttg	ttg	cat	gtt	cat	720
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
225					230				235					240		
aaa	aac	act	tat	gct	ctc	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	768
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	

42

tca gag act cgt gtc cca aac ggt cgg tcc taa
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

1521

<210> 24
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 252 amino acids from B. napus
 elongase KCS (SEQ ID NO:4); designated At254

<400> 24
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Leu Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
 165 170 175
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350

Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 25

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1002 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At173

<221> CDS

<222> (1)...(1518)

<400> 25

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	

100	105	110	
cgg aac gtg gca tgt gat gat Arg Asn Val Ala Cys Asp Asp 115	cgg tcc tcg ctc gat ttc ctg agg aag Pro Ser Ser Leu Asp Phe Leu Arg Lys 120		384
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly 130			432
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu 145			480
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc aag aac acc Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165			528
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 180			576
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195			624
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210			672
gcc gcc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225			720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245			768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260			816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Ser Asn Lys Pro Gly Asp Arg 275			864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290			912
gct gac gcc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305			960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325			1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340			1056

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tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt      1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
      355                      360                      365

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct      1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
      370                      375                      380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg      1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
      385                      390                      395                      400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga      1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
      405                      410                      415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat      1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420                      425                      430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa      1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435                      440                      445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt      1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450                      455                      460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa      1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
      465                      470                      475                      480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
      485                      490                      495

tca gag act cgt gtc cma aac ggt cgg tcc taa      1521
Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser
      500                      505

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<210> 26

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 173 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 333 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At173

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Pro or Gln

<400> 26

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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1           5           10           15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
      20           25           30

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47

WO 01/94565

PCT/US01/18737

<210> 27
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 528 bp from B. napus elongase KCS (SEQ ID NO:3)
 and 3' 993 bp from A. thaliana FAEL (SEQ ID NO:1);
 designated Bn176

<221> CDS
 <222> (1)...(1518)

<400> 27
 atg acg tcc att aac gta aag ctc ctt tac cat tac gtc ata acc aac 48
 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1 5 10 15
 ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa 96
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30
 gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt 192
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 ttc ggt tgc gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc 240
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc 288
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct 336
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110
 cgg aac ggc acg tgc gat gac tgc tgc tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag 480
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc 528
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg 576
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190

ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt	672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly	
245 250 255	
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt	816
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga	912
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gat gat gag agc	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser	
305 310 315 320	
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg	1008
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly	
325 330 335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct	1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt	1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu	
355 360 365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct	1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag	1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	
385 390 395 400	
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga	1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	


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gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa      1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435              440              445

gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt      1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450              455              460

tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa      1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
      465              470              475              480

cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
      485              490              495

tca aag act cat gtc caa aac ggt cgg tcc taa      1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser
      500              505

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<210> 28

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 176 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) and 3' 330 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2); designated Bn176

<400> 28

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Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1              5              10              15
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
      20              25              30
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
      35              40              45
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
      50              55              60
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
      65              70              75              80
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
      85              90              95
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
      100              105              110
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
      115              120              125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
      130              135              140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
      145              150              155              160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
      165              170              175
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
      180              185              190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
      195              200              205
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
      210              215              220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His

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225          230          235          240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
          245          250          255
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
          260          265          270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
          275          280          285
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
          290          295          300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
305          310          315          320
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
          325          330          335
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
          340          345          350
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
          355          360          365
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
          370          375          380
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
385          390          395          400
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
          405          410          415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
          420          425          430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
          435          440          445
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
          450          455          460
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
465          470          475          480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
          485          490          495
Ser Lys Thr His Val Gln Asn Gly Arg Ser
          500          505

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<210> 29

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 1197 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 324 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At399

<221> CDS

<222> (1)...(1518)

<400> 29

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1              5              10              15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
          20              25              30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc     144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
          35              40              45

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caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggc ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg	576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt	672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly	
245 250 255	
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt	816
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg	
275 280 285	

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aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga      912
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
290                               295                               300

gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc      960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
305                               310                               315                               320

ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg      1008
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
                               325                               330                               335

aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct      1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
                               340                               345                               350

tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt      1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
                               355                               360                               365

cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct      1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
                               370                               375                               380

gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gtg      1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385                               390                               395                               400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga      1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                               405                               410                               415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat      1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
                               420                               425                               430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa      1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                               435                               440                               445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt      1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                               450                               455                               460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa      1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465                               470                               475                               480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
                               485                               490                               495

tca gag act cgt gtc cma aac ggt cgg tcc taa      1521
Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser
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<210> 30

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 107 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At399

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Pro or Gln

<400> 30

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		20						25					30		
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55					60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65					70					75					80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser
			85						90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
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Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys
		115					120						125		
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly
	130					135					140				
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
145						150				155					160
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr
			165						170					175	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
		180					185						190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195					200						205			
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210				215						220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235					240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Gly
			245						250					255	
Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
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Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Ser	Gly	Asp	Arg
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Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290					295					300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser
305					310					315					320
Gly	Lys	Ile	Gly	Val	Cys	Leu	Ser	Lys	Asp	Ile	Thr	Asn	Val	Ala	Gly
			325						330					335	
Thr	Thr	Leu	Thr	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
		340						345					350		
Leu	Ser	Glu	Lys	Phe	Leu	Phe	Phe	Ala	Thr	Phe	Val	Ala	Lys	Lys	Leu
		355					360					365			
Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
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Val	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val
385					390					395					400

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Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr	Asn	
1				5					10					15		
ctt	ttc	aac	ctt	tgc	ttc	ttt	ccg	tta	acg	gcg	atc	gtc	gcc	gga	aaa	96
Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys	
			20					25					30			
gcc	tat	cgg	ctt	acc	ata	gac	gat	ctt	cac	cac	tta	tac	tat	tcc	tat	144
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr	
		35					40					45				
ctc	caa	cac	aac	ctc	ata	acc	atc	gct	cca	ctc	ttt	gcc	ttc	acc	gtt	192
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val	
	50					55					60					
ttc	ggt	tcg	gtt	ctc	tac	atc	gca	acc	cgg	ccc	aaa	ccg	gtt	tac	ctc	240
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	
65					70				75					80		
gtt	gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc	288
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	
				85					90					95		
tcc	aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	336
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	
		100						105					110			
cgg	aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	384
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 130 135 140	432
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag Leu Leu Gln Val Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 145 150 155 160	480
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 175	528
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	576
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gcc gcc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 255	768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac gcc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152

Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
 385 390 395 400
 cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga 1248
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt 1392
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa 1440
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
 465 470 475 480
 cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
 485 490 495
 tca aag act cat gtc caa aac ggt cgg tcc taa 1521
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
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<210> 32

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from *B. napus* elongase KCS (SEQ
 ID NO:3) and 3' 107 amino acids from *A. thaliana*
 FAE1 (SEQ ID NO:1); designated Bn399

<400> 32

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 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110


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Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
      115              120              125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
      130              135              140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
145              150              155              160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
      165              170              175
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
      180              185              190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
      195              200              205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
      210              215              220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225              230              235              240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
      245              250              255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
      260              265              270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
      275              280              285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
      290              295              300
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305              310              315              320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
      325              330              335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
      340              345              350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
      355              360              365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
      370              375              380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
385              390              395              400
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
      405              410              415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420              425              430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435              440              445
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450              455              460
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
465              470              475              480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
      485              490              495
Ser Lys Thr His Val Gln Asn Gly Arg Ser
      500              505

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<210> 33

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<223> 1524 bp from B. napus elongase KCS (SEQ ID NO:3)
 having a mutation at position 920; designated Bn
 G307D; hypothetical

WO 01/94565

PCT/US01/18737

<221> CDS

<222> (1)...(1518)

<400> 33

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ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa	96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys	
20 25 30	
gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat	144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr	
35 40 45	
ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt	192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val	
50 55 60	
ttc ggt tgc gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc	240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu	
65 70 75 80	
gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc	288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile	
85 90 95	
tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct	336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser	
100 105 110	
cgg aac ggc acg tgc gat gac tgc tgc tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tgc ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc gcc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tgc aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	

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465                               470                               475                               480
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
                               485                               490                               495

tca gag act cgt gtc caa aac ggt cgg tcc taataa                        1524
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
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<210> 34
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 506 amino acids from B. napus elongase KCS (SEQ ID
 NO:4) having a mutation at residue 307; designated
 Bn G307D; hypothetical

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<400> 34
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Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
                               20                               25                               30
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
                               35                               40                               45
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50                               55                               60
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
65                               70                               75                               80
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
                               85                               90                               95
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
                               100                              105                              110
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
                               115                              120                              125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130                              135                              140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
145                              150                              155                              160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
                               165                              170                              175
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
                               180                              185                              190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
                               195                              200                              205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210                              215                              220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225                              230                              235                              240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
                               245                              250                              255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
                               260                              265                              270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275                              280                              285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290                              295                              300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn

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305          310          315          320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
          325          330          335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
          340          345          350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
          355          360          365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
          370          375          380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385          390          395          400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
          405          410          415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
          420          425          430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
          435          440          445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
          450          455          460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465          470          475          480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
          485          490          495
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
          500          505

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<210> 35

<211> 1709

<212> DNA

<213> Artificial Sequence

<220>

<223> 1709 bp from A. thaliana FAEL (SEQ ID NO:1) having
a mutation at position 275; designated At K92R;
hypothetical

<221> CDS

<222> (1)...(1518)

<400> 35

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1              5              10              15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
          20              25              30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
          35              40              45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
          50              55              60

ggc ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt      240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
          65              70              75              80

gac tac tcg tgt tac ctt cca cca ccg cat ctc aga gtt agt gtc tct      288

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Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg	576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt	672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly	
245 250 255	
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt	816
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga	912
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser	
305 310 315 320	
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg	1008
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly	

325	330	335	
aca aca ctt acg aaa aat ata gca	aca ttg ggt ccg ttg att ctt cct		1056
Thr Thr Leu Thr Lys Asn Ile Ala	Thr Leu Gly Pro Leu Ile Leu Pro		
340	345	350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt			1104
Leu Ser Glu Lys Phe Leu Phe Phe	Ala Thr Phe Val Ala Lys Lys Leu		
355	360	365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct			1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr	Val Pro Asp Phe Lys Leu Ala		
370	375	380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag			1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu			
385	390	395	400
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga			1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat			1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr			
420	425	430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa			1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt			1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa			1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln			
465	470	475	480
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag			1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys			
485	490	495	
tca aag act cat gtc caa aac ggt cgg tcc taatttgatg tatctgagtg			1538
Ser Lys Thr His Val Gln Asn Gly Arg Ser			
500	505		
ccaacgttta ctttgccttt cctttctttt attggttatg aattagatgt ttactaatgt			1598
tcctctcttt ttcggtataa ataaagaagt tcaattcttc ctatagtttc aaacgcgatt			1658
ttaagcgctt ctatttaggt ttacatgaat ttctttttaca aaccatcttt t			1709
<210> 36			
<211> 506			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> 506 amino acids from A. thaliana FAE1 (SEQ ID			
NO:2) having a mutation at residue 92; designated			
At K92R; hypothetical			
<400> 36			

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	1	5	10	15
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	20	25	30	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	35	40	45	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	50	55	60	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	65	70	75	80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser	85	90	95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	100	105	110	
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	130	135	140	
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	145	150	155	160
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr	165	170	175	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205	
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Gly	245	250	255	
Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Ser	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser	305	310	315	320
Gly	Lys	Ile	Gly	Val	Cys	Leu	Ser	Lys	Asp	Ile	Thr	Asn	Val	Ala	Gly	325	330	335	
Thr	Thr	Leu	Thr	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	340	345	350	
Leu	Ser	Glu	Lys	Phe	Leu	Phe	Phe	Ala	Thr	Phe	Val	Ala	Lys	Lys	Leu	355	360	365	
Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	370	375	380	
Val	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu	385	390	395	400
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	405	410	415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	420	425	430	
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	435	440	445	
Ala	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	450	455	460	
Trp	Val	Ala	Leu	Arg	Asn	Val	Lys	Ala	Ser	Ala	Asn	Ser	Pro	Trp	Gln	465	470	475	480
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Leu	Ser	Lys				

485 490 495
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

<210> 37
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 762 bp from A. thaliana FAEL (SEQ ID NO:1) and
 3' 759 bp from B. napus elongase KCS (SEQ ID NO:3)
 and having a mutation at position 920; designated
 At254 G307D; hypothetical

<221> CDS
 <222> (1)...(1518)

<400> 37
 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct 288
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag 384
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125
 att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140
 ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag 480
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160
 aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc 528
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr

165	170	175	
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg			576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag			624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt			672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat			720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aac act tat gct ctc gtg gtg agc aca gag aac atc act tat aac			768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc			816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt			864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga			912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac			960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt			1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg			1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt			1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
355	360	365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct			1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg			1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga			1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
tca gag act cgt gtc caa aac ggt cgg tcc taa	1521
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser	
500 505	

<210> 38

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 252 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated At254 G307D; hypothetical

<400> 38

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ser Arg Glu Glu	
145 150 155 160	
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	

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      180      185      190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
      195      200      205
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
      210      215      220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225      230      235      240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
      245      250      255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
      260      265      270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
      275      280      285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
      290      295      300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305      310      315      320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
      325      330      335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
      340      345      350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
      355      360      365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
      370      375      380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385      390      395      400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
      405      410      415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420      425      430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435      440      445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450      455      460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465      470      475      480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
      485      490      495
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
      500      505

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<210> 39

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 519 bp from A. thaliana FAEL (SEQ ID NO:1) and
 3' 1002 bp from B. napus elongase KCS (SEQ ID
 NO:3) and having a mutation at position 920;
 designated At173 G307D

<221> CDS

<222> (1)...(1518)

<400> 39

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1              5              10              15

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48

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc aag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816

Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
tca gag act cgt gtc caa aac ggt cgg tcc taa	1521
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser	

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500

505

<210> 40

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 173 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 333 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated At173 G307D; hypothetical

<400> 40

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		20						25				30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35				40					45				
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50				55					60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65				70				75						80	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser
			85					90					95		
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
		100						105					110		
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly
	130				135					140					
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
145				150					155					160	
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165					170					175		
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
		180						185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195					200						205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210				215					220					
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225				230					235					240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245					250					255		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
		260						265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
	275					280					285				
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290				295					300					
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305				310					315					320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325					330					335		
Arg	Thr	Val	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
		340					345					350			
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu
	355					360						365			

Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 41

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 1197 bp from B. napus elongase KCS (SEQ ID
 NO:3) and 3' 324 bp from A. thaliana FAEL (SEQ ID
 NO:1) and having a mutation at nucleotide position
 920; designated Bn399 G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 41

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1 5 10 15	
ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa	96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys	
20 25 30	
gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat	144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr	
35 40 45	
ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt	192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val	
50 55 60	
ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc	240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu	
65 70 75 80	
gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc	288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile	
85 90 95	
tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct	336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser	
100 105 110	

cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt cgg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	

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tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt      1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
      355                      360                      365

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct      1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
      370                      375                      380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag      1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
      385                      390                      395                      400

cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga      1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
      405                      410                      415

tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat      1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420                      425                      430

gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa      1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435                      440                      445

gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt      1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450                      455                      460

tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa      1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
      465                      470                      475                      480

cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
      485                      490                      495

tca aag act cat gtc caa aac ggt cgg tcc taa                          1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser
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<210> 42

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from B. napus elongase KCS (SEQ ID NO:3) and 3' 107 amino acids from A. thaliana FAEL (SEQ ID NO:1) having a mutation at residue 306; designated Bn399 G307D; hypothetical

<400> 42

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Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1           5           10           15
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
      20           25           30
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
      35           40           45
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
      50           55           60

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Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	65	70	75	80
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	85	90	95	
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	100	105	110	
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	130	135	140	
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	145	150	155	160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	165	170	175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205	
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	245	250	255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	305	310	315	320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	325	330	335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	340	345	350	
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	355	360	365	
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	370	375	380	
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu	385	390	395	400
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	405	410	415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	420	425	430	
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	435	440	445	
Ala	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	450	455	460	
Trp	Val	Ala	Leu	Arg	Asn	Val	Lys	Ala	Ser	Ala	Asn	Ser	Pro	Trp	Gln	465	470	475	480
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Leu	Ser	Lys	485	490	495	
Ser	Lys	Thr	His	Val	Gln	Asn	Gly	Arg	Ser							500	505		

<210> 43

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
 <223> primer for PCR

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 <210> 44
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 <400> 44
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 <210> 45
 <211> 28
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 <400> 45
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 <210> 46
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 ccgcattgca gagttagtgt ctctaaa 27

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 <210> 51
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 <400> 51
 ccaccgcata tcagagttag tgtctct 27

 <210> 52
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 agagacacta actctgagat gcggtgg 27

 <210> 53
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 <400> 53
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 <210> 54
 <211> 31
 <212> DNA
 <213> Artificial Sequence

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<220>

<223> primer for PCR

<400> 54

ccgaattcctt aggaccgacc gttttggaca c

31

<210> 55

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 55

ggggatccat gacgtccatt aacgtaaagc tcc

33

<210> 56

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 56

ccgaattcctt aggaccgacc gttttggaca tgagtctt

38

WHAT IS CLAIMED IS:

1. A polypeptide comprising in the amino-terminal to carboxy-terminal direction:
 - 5 (a) a first polypeptide segment, wherein said first polypeptide segment has membrane anchoring properties; joined to
 - (b) a second polypeptide segment having a sequence selected from the group consisting of residues 75-114 of SEQ ID NO:12 and residues 75-114 of SEQ ID NO:14; joined to
 - 10 (c) a third polypeptide segment having at least 40% sequence identity to residues 115-506 of SEQ ID NO:4.
2. The polypeptide of claim 1, wherein said third polypeptide segment has at least 50% sequence identity to residues 115-506 of SEQ ID NO:4.
- 15 3. The polypeptide of claim 2, wherein said third polypeptide segment has an aspartic acid at the position corresponding to amino acid 307 of SEQ ID NO:4.
4. The polypeptide of claim 3, wherein said polypeptide has the amino acid
20 sequence of SEQ ID NO:20.
5. The polypeptide of claim 3, wherein said polypeptide has the amino acid sequence of SEQ ID NO:22.
- 25 6. The polypeptide of claim 3, wherein said polypeptide has the amino acid sequence of SEQ ID NO:34.
7. The polypeptide of claim 3, wherein said polypeptide has the amino acid sequence of SEQ ID NO:36.

30

8. The polypeptide of claim 1, wherein said polypeptide catalyzes the condensation of malonyl CoA and a C18 fatty acyl substrate, leading to the synthesis of a C20 fatty acyl CoA.

5 9. The polypeptide of claim 8, wherein said C18 fatty acyl substrate is an oleoyl substrate.

10 10. The polypeptide of claim 1, wherein said polypeptide catalyzes the condensation of malonyl CoA and a C20 fatty acyl substrate, leading to the synthesis of a C22 fatty acyl CoA.

11. The polypeptide of claim 10, wherein said C20 fatty acyl substrate is an eicosenoyl substrate.

15 12. A nucleic acid encoding the polypeptide of claim 1.

13. A nucleic acid encoding the polypeptide of claim 2.

14. A nucleic acid encoding the polypeptide of claim 3.

20

15. Host cells containing a nucleic acid encoding the polypeptide of claim 1.

16. Host cells containing a nucleic acid encoding the polypeptide of claim 2.

25 17. Host cells containing a nucleic acid encoding the polypeptide of claim 3.

18. The host cells of claim 15, wherein said host cells are yeast cells.

19. The host cells of claim 15, wherein said host cells are plant cells.

30

20. A plant containing an exogenous nucleic acid encoding the polypeptide of claim 1.
21. A plant containing an exogenous nucleic acid encoding the polypeptide of claim 2.
22. A plant containing an exogenous nucleic acid encoding the polypeptide of claim 3.
23. The plant of claim 20, wherein said plant is *Brassica napus*.
24. The plant of claim 21, wherein said plant is *Brassica napus*.
25. The plant of claim 22, wherein said plant is *Brassica napus*.

Arabidopsis thaliana FAE1 (SEQ ID NO:2)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LKVSVSKVMD
 IFYQIRKADT SSRNVACDDP SSLDFLRKIQ ERSGLGDETY SPEGLIHVPP
 RKTFAASREE TEKVIIGALE NLFENTKVNP REIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNIKSFNLGG MGCSAGVIAI DLAKDLLHVH KNTYALVVST
 ENITQGIYAG ENRSMMSVNC LFRVGGAAIL LSNKSGDRRR SKYKLVHTVR
 THTGADDKSF RCVQQEDDES GKIGVCLSKD ITNVAGTTLT KNIATLGPLI
 LPLSEKFLFF ATFVAKKLLK DKIKHYVPD FKLAVDHFCI HAGGRAVIDE
 LEKNLGLSPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKKGKNKAW
 QIALGSGFKC NSAVWVALRN VKASANSWPQ HCIDRYPVKI DSDLKSKTH
 VQNGRS

Brassica napus elongase KCS (SEQ ID NO:4)

MTSINVKLLY HYVITNLFNL CFFPLTAIVA GKAYRLTIDD LHHLYYSYLQ
 HNLITIAPLF AFTVFGSVLY IATRPKPVYL VEYSCYLPPT HCRSSISKVM
 DIFYQVRKAD PSRNGTCDDS SWLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAKDLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMSVNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADGKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFF DKIKHYVPD FKLAI DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKKGKNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VQNGRS

B. napus elongase KCS (SEQ ID NO:6)

MTSINVKLLY HYVITNLFNL CFFPLTAIVA GKAYLTIDDL HHLIYSYLQH
 NLITIAPLLA FTVFGSVLYI ATRPKPVYLV EYSCYLPPTH CRSSISKVMD
 IFFQVRKADP SRNGTCDDSS WLDFLRKIQE RSGLGDETHG PEGLLQVPPR
 KTFARAREET EQVIIGALEN LFKNTNVNPK DIGILVVNSS MFNPTPSLSA
 MVVNTFKLRS NVRSFNLGGM GCSAGVIAID LAKDLLHVHK NTYALVVSTE
 NITYNIYAGD NRSMMVSNC LFRVGGAAIL SNKPRDRRRS KYELVHTVRT
 HTGADDKSFR CVQQGDDENG QTGVSLSKDI TDVAGRTVKK NIATLGPLIL
 PLSEKLLFFV TFMGKKLFD EIKHYVPDF KLAI DHFCIH AGGKAVIDVL
 EKNLGLAPID VEASRSTLHR FGNTSSSSIW YELAYIEPKG RMKKGNKVWQ
 IALGSGFKCN SAVWVALNNV KASTNSPWEH CIDRYPVKID SDSGKSETRV
 PNGRS

FIGURE 1-1

At114 (SEQ ID NO:8)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LKVS SVSKVMD
 IFYQIRKADT SSRNGTCDD S WLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAKDLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMVSNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADGKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYYPVD FKLAIDHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VPNGRS

At74 (SEQ ID NO:10)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPKPVYLV EYSCYLPPPH CRSSISKVMD
 IFYQVRKADP SRNGTCDDSS WLDFLRKIQE RSGGLGDETHG PEGLLQVPPR
 KTFAAAAREET EQVIIGALEN LFKNTNVNPK DIGILVVNSS MFNPTPSLSA
 MVVNTFKLRS NVRSFNLGGM GCSAGVIAID LAKDLLHVHK NTYALVVSTE
 NITYNIYAGD NRSMMVSNC LFRVGGAAILL SNKPGDRRRS KYELVHTVRT
 HTGADGKSFR CVQQGDDENG KIGVSLSKDI TDVAGRTVKK NIATLGPLIL
 PLSEKLLFFV TFMGKKLFKD KIKHYYPDF KLAIDHFCIH AGGRAVIDVL
 EKNLALAPID VEASRSTLHR FGNTSSSSIW YELAYIEAKG RMKGKGNKVWQ
 IALGSGFKCN SAVWVALNNV KASTNSPWEH CIDRYPVKID SDSGKSETRV
 QNGRS

At114 L91C K92R (SEQ ID NO:12)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH **CRVSVSKVMD**
 IFYQIRKADT SSRNGTCDNS WLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAKDLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMVSNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADGKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYYPVD FKLAIDHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VPNGRS

FIGURE 1-2

At114 K92R (SEQ ID NO:14)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LRVSVSKVMD
 IFYQIRKADT SSRNGTCDDDS SWLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAKDLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMSVNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADGKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYVPD FKLAI DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VPNGRS

At114 G307D (SEQ ID NO:16)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LKVS SVSKVMD
 IFYQIRKADT SSRNGTCDDDS SWLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAKDLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMSVNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADGKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYVPD FKLAI DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VQNGRS

At74 G306D (SEQ ID NO:18)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPKPVYLV EYSCYLPPTH CRSSISKVMD
 IFYQVRKADP SRNGTCDDSS WLDLFLRKIQE RSGLGDETHG PEGLLQVPPR
 KTFAAAREET EQVIIGALEN LFKNTNVNPK DIGILVVNSS MFNPTPSLSA
 MVVNTFKLRS NVRSFNLGGM GCSAGVIAID LAKDLLHVHK NTYALVVSTE
 NITYNIYAGD NRSMMVSNCL FRVGGAAILL SNKPGDRRRS KYELVHTVRT
 HTGADGKSF CVQQGDDENG KIGVSLSKDI TDVAGRTVKK NIATLGPLIL
 PLSEKLLFFV TFMGKKLFKD KIKHYVPDF KLAI DHFCIH AGGRAVIDVL
 EKNLALAPID VEASRSTLHR FGNTSSSSIW YELAYIEAKG RMKGKNKVWQ
 IALGSGFKCN SAVWVALNNV KASTNSPWEH CIDRYPVKID SDSGKSETRV
 QNGRS

FIGURE 1-3

At114 L91C K92R G307D (SEQ ID NO:20)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH **CRVSVSKVMD**
 IFYQIRKADT SSRNGTCDNS SWLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAkdLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMSVNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGAD**DK**SF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYVPD FKLAI DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VQNGRS

At114 K92R G307D (SEQ ID NO:22)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH **LRVSVSKVMD**
 IFYQIRKADT SSRNGTCDD SSWLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAkdLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMSVNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGAD**DK**SF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYVPD FKLAI DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VQNGRS

At254 (SEQ ID NO:24)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNLLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LKVSVSKVMD
 IFYQIRKADT SSRNVACDDP SSLDFLRKIQ ERSGLGDETY SPEGLIHVPP
 RKTFAASREE TEKVIIGALE NLFENTKVNP REIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNIKSFNLGG MGCSAGVIAI DLAkdLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMSVNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADGKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYVPD FKLAI DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VPNGRS

FIGURE 1-4

At173 (SEQ ID NO:26)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LKVSVSKVMD
 IFYQIRKADT SSRNVACDDP SSLDFLRKIQ ERSGLGDETY SPEGLIHVPP
 RKTFAASREE TEKVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSENLGG MGCSAGVIAI DLAkdLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMVSNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADGKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFF DKIKHYYPV FKLAI DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMCKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCDRYPVKI DSDSGKSETR
 VQNGRS

Bn176 (SEQ ID NO:28)

MTSINVKLLY HYVITNLENL CFFPLTAIVA GKAYRLTIDD LHHLYYSYLQ
 HNLITIAPLF AFTVFGSVLY IATRPKPVYL VEYSCYLPPPT HCRSSISKVM
 DIFYQVRKAD PSRNGTCDD SLDWFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAREE TEQVIIGALE NLFKNTKVNP REIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNIKSENLGG MGCSAGVIAI DLAkdLLHVH KNTYALVVST
 ENITQGIYAG ENRSMMVSNC LFRVGGAAIL LSNKSGDRRR SKYKLVTHTV
 THTGADDKSF RCVQQEDDES GKIGVCLSKD ITNVAGTTLT KNIATLGPLI
 LPLSEKFLFF ATFVAKKLLK DKIKHYYPV FKLAV DHFCI HAGGRAVIDE
 LEKNLGLSPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMCKGNKAW
 QIALGSGFKC NSAVWVALRN VKASANSWPQ HCDRYPVKI DSDLSKSKTH
 VQNGRS

At399 (SEQ ID NO:30)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LKVSVSKVMD
 IFYQIRKADT SSRNVACDDP SSLDFLRKIQ ERSGLGDETY SPEGLIHVPP
 RKTFAASREE TEKVIIGALE NLFENTKVNP REIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNIKSENLGG MGCSAGVIAI DLAkdLLHVH KNTYALVVST
 ENITQGIYAG ENRSMMVSNC LFRVGGAAIL LSNKSGDRRR SKYKLVTHTV
 THTGADDKSF RCVQQEDDES GKIGVCLSKD ITNVAGTTLT KNIATLGPLI
 LPLSEKFLFF ATFVAKKLLK DKIKHYYPV FKLAV DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMCKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCDRYPVKI DSDSGKSETR
 VQNGRS

FIGURE 1-5

Bn399 (SEQ ID NO:32)

MTSINVKLLY HYVITNLENL CFFPLTAIVA GKAYRLTIDD LHHLYYSYLQ
 HNLITIAPLF AFTVFGSVLY IATRPKPVYL VEYSCYLPPT HCRSSISKVM
 DIFYQVRKAD PSRNGTCDDS SWLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAKDLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMVSNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADGKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFF DKIKHYVPD FKLAIDHFCI HAGGRAVIDE
 LEKNLGLSPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKAW
 QIALGSGFKC NSAVWVALRN VKASANSPWQ HCIDRYPVKI DSDLKSKTH
 VQNGRS

Bn G307D (SEQ ID NO:34)

MTSINVKLLY HYVITNLENL CFFPLTAIVA GKAYRLTIDD LHHLYYSYLQ
 HNLITIAPLF AFTVFGSVLY IATRPKPVYL VEYSCYLPPT HCRSSISKVM
 DIFYQVRKAD PSRNGTCDDS SWLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAKDLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMVSNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADDKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFF DKIKHYVPD FKLAIDHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VQNGRS

At K92R (SEQ ID NO:36)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LRVSVSKVMD
 IFYQIRKADT SSRNVACDDP SSLDFLRKIQ ERSGLGDETY SPEGLIHVPP
 RKTFAASREE TEKVIIGALE NLFENTKVNP REIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNIKSFNLGG MGCSAGVIAI DLAKDLLHVH KNTYALVVST
 ENITQGIYAG ENRSMMVSNC LFRVGGAAIL LSNKSGDRRR SKYKLVHTVR
 THTGADDKSF RCVQQEDDES GKIGVCLSKD ITNVAGTTLT KNIATLGPLI
 LPLSEKFLFF ATEVAKKLLK DKIKHYVPD FKLAVDHFCI HAGGRAVIDE
 LEKNLGLSPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKAW
 QIALGSGFKC NSAVWVALRN VKASANSPWQ HCIDRYPVKI DSDLKSKTH
 VQNGRS

FIGURE 1-6

At254 G307D (SEQ ID NO:38)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LKVSVSKVMD
 IFYQIRKADT SSRNVACDDP SSLDFLRKIQ ERSGLGDETY SPEGLIHVPP
 RKTFAASREE TEKVIIGALE NLFENTKVNP REIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNIKSFNLGG MGCSAGVIAI DLAkdLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMSVNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADDKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYVPD FKLAI DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VQNGRS

At173 G307D (SEQ ID NO:40)

MTSVNVKLLY RYVLTNFFNL CLFPLTAFLA GKASRLTIND LHNFLSYLQH
 NLITVTLLFA FTVFGLVLYI VTRPNPVYLV DYSCYLPPPH LKVSVSKVMD
 IFYQIRKADT SSRNVACDDP SSLDFLRKIQ ERSGLGDETY SPEGLIHVPP
 RKTFAASREE TEKVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAkdLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMSVNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADDKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYVPD FKLAI DHFCI HAGGRAVIDV
 LEKNLALAPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKVW
 QIALGSGFKC NSAVWVALNN VKASTNSPWE HCIDRYPVKI DSDSGKSETR
 VQNGRS

Bn399 G307D (SEQ ID NO:42)

MTSINVKLLY HYVITNLFNL CFFPLTAIVA GKAYRLTIDD LHHLYYSYLQ
 HNLITIAPLF AFTVFGSVLY IATRPKPVYL VEYSCYLPPT HCRSSISKVM
 DIFYQVRKAD PSRNGTCDDS SWLDFLRKIQ ERSGLGDETH GPEGLLQVPP
 RKTFAAAREE TEQVIIGALE NLFKNTNVNP KDIGILVVNS SMFNPTPSLS
 AMVVNTFKLR SNVRSFNLGG MGCSAGVIAI DLAkdLLHVH KNTYALVVST
 ENITYNIYAG DNRSMMSVNC LFRVGGAAIL LSNKPGDRRR SKYELVHTVR
 THTGADDKSF RCVQQGDDEN GKIGVSLSKD ITDVAGRTVK KNIATLGPLI
 LPLSEKLLFF VTFMGKKLFK DKIKHYVPD FKLAI DHFCI HAGGRAVIDE
 LEKNLGLSPI DVEASRSTLH RFGNTSSSSI WYELAYIEAK GRMKGKGNKAW
 QIALGSGFKC NSAVWVALRN VKASANS PWQ HCIDRYPVKI DSDLKSKETH
 VQNGRS

FIGURE 1-7

60043919.doc

Arabidopsis thaliana FAE1 (SEQ ID NO:1)

atgacgtccg ttaacgttaa gctcctttac cgttacgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctgggcttac cataaacgat ctccacaact tcctttccta tctccaacac
 aaccttataa cagtaacttt actctttgct ttcaactgtt tcggtttggt
 tctctacatc gtaaccggac ccaatccggc ttatctcggt gactactcgt
 gttaccttcc accacggcat ctcaaagtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg
 tgatgatccg tcctcgctcg atttctgag gaagattcaa gagcggtcag
 gtctagggtga tgagacgtac agtctgagg gactcattca cgtaccaccg
 cggagactt ttgcagcgtc acgtgaagag acagagaagg ttatcatcgg
 tgcgctcgaa aatctattcg agaacaccaa agttaaccct agagagattg
 gtatacttgt ggtgaactca agcatgttta atccaactcc ttcgctatcc
 gctatggctg ttaatacttt caagctccga agcaacatca aaagctttaa
 tctaggagga atgggttgta gtgctgggtg tattgccatt gatttggcta
 aagacttggt gcatgttcat aaaaacactt atgctcttgt ggtgagcact
 gagaacatca cacaaggcat ttatgctgga gaaaatagat caatgatggt
 tagcaattgc ttgtttcgtg ttggtggggc cgcgattttg ctctctaaca
 agtcgggaga cgggagacgg tccaagtaca agctagtcca cacggtcoga
 acgcatactg gagctgatga caagtctttt cgatgtgtgc aacaagaaga
 cgatgagagc ggcaaaatcg gagtgtgtct gtcaaaggac ataaccaatg
 ttgcgggggac aacacttacg aaaaatatag caacattggg tccgttgatt
 cttcctttaa gcgaaaagtt tctttttttc gctaccttcg tcgccaagaa
 acttctaaag gataaaatca agcattacta tgttcgggat ttcaagcttg
 ctgttgacca tttctgtatt catgccggag gcagagccgt gatcgatgag
 ctagagaaga acttaggact atcccgatc gatgtggagg catctagatc
 aacgttacat agatttggga atacttcac tagctcaatt tggatgaat
 tagcatacat agaggcaaag ggaagaatga agaaagggaa taaagcttgg
 cagattgctt taggatcagg gtttaagtgt aatagtgcgg tttgggtggc
 tctacgcaat gtcaaggcat cggcaaatag tccttggcaa cattgcatcg
 atagatatcc ggttaaaatt gattctgatt tgtcaaagtc aaagactcat
 gtccaaaacg gtcggctcta atttgatga tctgagtgcc aacgtttact
 ttgtctttcc tttcttttat tggttatgaa ttagatgttt actaatgttc
 ctctcttttt cgttataaat aaagaagttc aattcttcct atagtttcaa
 acgcgatttt aagcgtttct atttaggttt acatgaattt cttttacaaa
 ccatctttt

FIGURE 2-1

Brassica napus elongase KCS (SEQ ID NO:3)

```

atgacgtcca ttaacgtaaa gctccttttac cattacgtca taaccaacct
tttcaacctt tgcttctttc cgttaacggc gatcgtcgcc ggaaaagcct
atcggcttac catagacgat cttcaccact tatactattc ctatctccaa
cacaacctca taaccatcgc tccactcttt gccttcaccg ttttcgggtc
ggttctctac atcgcaaccg ggcccaaacg ggtttacctc gttgagtact
catgctacct tccaccaacg cattgtagat caagtatctc caaggtcattg
gatatctttt atcaagtaag aaaagctgat ccttctcggg acggcacgtg
cgatgactcg tcgtggcttg acttcttgag gaagattcaa gaacggtcag
gtctaggcga tgaaactcac gggcccgagg ggctgcttca ggtccctccc
cggaagactt ttgcggcggc gcgtgaagag acggagcaag ttatcattgg
tgcgctagaa aatctattca agaacaccaa cgttaaccct aaagatatag
gtatacttgt ggtgaactca agcatgttta atccaaactcc atcgtctctcc
gcgatggctg ttaacacttt caagctccga agcaacgtaa gaagctttta
ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
gagaacatca cttataacat ttacgctggg gataataggt ccatgatggg
ttcaaattgc ttgttcogtg ttggtggggc cgctattttg ctctccaaca
agcctggaga tcgtagacgg tccaagtacg agctagtcca cacgggttcga
acgcataccg gagctgacgg caagtctttt cgttgcgtgc aacaaggaga
cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
ttgctggctg aacggttaag aaaaacatag caacgttggg tccgttgatt
cttcogttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
ctagagaaga acctagccct agcacccgac gatgtagagg catcaagatc
aacggttacat agatttgga acacttcac tagctcaata tggatgagt
tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
tctaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
gtccaaaacg gtcggtccta ataa

```

FIGURE 2-2

B. napus elongase KCS (SEQ ID NO:5)

```

tagagcgtaa  cggaccacaa  aagaggatcc  atacaaatac  atctcatcgc
ttccattact  attctccgac  acacacactg  agcaatgacg  tccattaacg
taaagctcct  ttaccattac  gtcataacca  accttttcaa  cctttgtttc
tttccattaa  cggcgatcgt  cgccggaaaa  gcctatctta  ccatagacga
tcttcaccac  ttatactatt  cctatctcca  acacaacctc  ataaccattg
ctccactctt  ggccttcacc  gttttcgggt  cggttctcta  catcgcaacc
cggcccaaac  cggtttacct  cgtggagtag  tcatgctacc  ttccaccaac
gcattgtaga  tcaagtatct  ccaaggtagc  ggatatcttt  ttccaagtaa
gaaaagctga  tccttctcgg  aacggcacgt  gcgatgactc  gtcctggcct
gacttcttga  ggaagattca  agaacggtca  ggtctaggcg  atgaaacca
cgggcccag  gggctgcttc  aggtccctcc  ccggaagact  tttgcgcgcg
cgcgtgaaga  gacggagcaa  gttatcattg  gtgcgctaga  aaatctattc
aagaacacca  atgttaacct  taaagatata  ggtatacttg  tggatgaactc
aagcatgttt  aatccaactc  ctctgccttc  cgcgatgggc  gttaacactt
tcaagctccg  aagcaacgta  agaagcttta  accttggtgg  catgggttgt
agtgcggcg  ttatagccat  tgatctagca  aaggacttgt  tgcattgtcca
taaaaatacg  tatgctcttg  tggtagcac  agagaacatc  acttataaca
tttacgctgg  tgataatagg  tccatgatgg  tttcaaattg  cttgttccgt
gttggtggg  ccgctatttt  gctctccaac  aagcctagag  atcgtagacg
gtccaagtac  gagctagttc  acacggttcg  aacgcatacc  ggagctgacg
acaagtcttt  tcggtgcgtg  caacaaggag  acgatgagaa  cggccaaacc
ggagtgagtt  tgtccaagga  cataaccgat  gttgctgggc  gaacgggtta
gaaaaacata  gcaacgctgg  gtcggttgat  tcttccgtta  agcgagaaac
ttcttttttt  cgttaccttc  atgggcaaga  aacttttcaa  agacgaaatc
aaacattatt  acgtcccggg  ctccaagctt  gctatcgacc  atttttgtat
acatgccgga  ggcaaagccg  tgattgatgt  gctagagaag  aacctaggcc
tagcaccgat  cgatgtagag  gcatcaagat  caacggtaca  tagatttggg
aacacttcat  ctagctcaat  atggtatgag  ttggcataca  tagaacccaa
aggaaggatg  aagaaaggta  ataaagtttg  gcagattgct  ttagggctag
gctttaagtg  taacagtgca  gtttggtgg  ctctaaacaa  tgtcaaagct
tcaacaaata  gtccttgga  aactgcctc  gacagatacc  cggttaaaat
tgattctgat  tcaggtaagt  cagagactcg  tgtcccaaac  ggctcgctct
aataaatgat  gtttgctctc  tttcgtttct  ttttattggg  tataataatt
tgatggccac  gatgtttctc  ttgtttgtta  tgaataaaga  atcccacggt
gttctagtaa  aaaaaaaaaa  aaaaaaaaaa  aaaaaa

```

FIGURE 2-3

At114 (SEQ ID NO:7)

atgacgtccg ttaacgttaa gctcctttac cgttatgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctcggtttac cataaacgat ctccacaact tcctttccta tctccaacac
 aaccttataa cagtaacttt actctttgct ttcactgttt tcggtttggt
 tctctacatc gtaacccgac ccaatccggt ttatctcggt gactactcgt
 gttaccttcc gccaccgcat ctcaaagtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acggcacgtg
 tgatgattcg tcgtggcttg acttcttgag gaagattcaa gaacgttcag
 gtctaggcga tgaaactcac gggcccagag ggctgcttca ggtccctccc
 cggaagactt ttgcggcggc gcgtgaagag acggagcaag ttatcattgg
 tgcgctagaa aatctattca agaacaccaa cgttaaccct aaagatatag
 gtatacttgt ggtgaactca agcatgttta atccaactcc atcgctctcc
 gcgatggctg ttaacacttt caagctccga agcaacgtaa gaagctttaa
 ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
 aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
 gagaacatca cttataacat ttacgctggt gataataggt ccatgatggt
 ttcaaattgc ttgttccgtg ttggtggggc cgctattttg ctctccaaca
 agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
 acgcataccg gagctgacgg caagtctttt cgttgcgtgc aacaaggaga
 cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
 ttgctggctg aacggttaag aaaaacatag caacgttggg tccgttgatt
 cttccgttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
 acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
 ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
 ctagagaaga acctagccct agcaccgac gatgtagagg catcaagatc
 aacgttacat agatttgga acacttcac tagctcaata tggatgagt
 tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
 cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
 tctaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgt
 acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
 gtcccaaacg gtcggtccta a

FIGURE 2-4

At74 (SEQ ID NO:9)

```

atgacgtccg ttaacgttaa gctcctttac cgttacgtct taaccaactt
tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
ctcggcttac cataaacgat ctccacaact tcttttccta tctccaacac
aaccttataa cagtaacttt actctttgct ttcactgttt tcggtttggt
tctctacatc gtaacccgac ccaaaccggt ttacctcggt gagtactcat
gctaccttcc accaacgcat tgtagatcaa gtatctccaa ggtcatggat
atcttttata aagtaagaaa agctgaccc tctcggaacg gcacgtgcga
tgactcgctc tggcttgact tcttgaggaa gattcaagaa cgttcaggtc
taggcgatga aactcacggg ccgaggggc tgcttcaggc cctccccgg
aagacttttg cggcggcgcg tgaagagacg gagcaagtta tcattggtgc
gctagaaaat ctattcaaga acaccaacgt taaccctaaa gatataggta
tacttggtgt gaactcaagc atgttttaac caactccatc gctctccgcg
atggtcgtta acactttcaa gctccgaagc aacgtaagaa gctttaacct
tggtggcatg ggttgtagtg ccggcggtat agccattgat ctagcaaagg
acttggttgc tgtccataaa aatacgtatg ctcttggtgt gagcacagag
aacatcactt ataacattta cgtcggtgat aatagggtcc tgatggtttc
aaattgcttg ttccgtgttg gtggggccgc tattttgctc tccaacaagc
ctggagatcg tagacgggtc aagtacgagc tagttcacac ggttcgaacg
cataccggag ctgacggcaa gtcttttcgt tgcttgcaac aaggagacga
tgagaacggc aaaatcggag tgagtttgtc caaggacata accgatgttg
ctggtcgaac ggttaagaaa aacatagcaa cgttggggtc gttgattctt
ccgttaagcg agaaacttct ttttttcgtt accttcattg gcaagaaact
tttcaaagat aaaatcaaac attactacgt ccgggatttc aaacttgcta
ttgaccattt ttgtatacat gccggaggca gagccgtgat tgatgtgcta
gagaagaacc tagccctagc accgatcgat gtagaggcat caagatcaac
gttacataga tttggaaaca cttcatctag ctcaatatgg tatgagttgg
catacataga agcaaaagga aggatgaaga aaggtaataa agtttggcag
attgctttag ggtcaggctt taagtgtaac agtgcagttt ggggtggctct
aaacaatgtc aaagcttcga caaatagtcc ttgggaacac tgcacgcaca
gatacccggt caaaattgat tctgattcag gtaagtcaga gactcgtgtc
caaaacggtc ggtcctaa

```

FIGURE 2-5

At114 L91C K92R (SEQ ID NO:11)

atgacgtccg ttaacgttaa gctcctttac cgttatgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctcggttac cataaacgat ctccacaact tcctttccta tctccaacac
 aacctataa cagtaacttt actctttgct ttcactgttt tcggtttggg
 tctctacatc gtaaccgcac ccaatccggg ttatctcggt gactactcgt
 gttaccttcc gccaccgcat **tgacagag**tta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acggcacgtg
 tgataattcg tcgtggcctg acttcttgag gaagattcaa gaacgttcag
 gtctaggcga tgaaactcac gggcccaggg ggctgcttca ggtccctccc
 cggaagactt ttgcggcggc gcgtgaagag acggagcaag ttatcattgg
 tgcgctagaa aatctattca agaacaccaa cgttaacctt aaagatatag
 gtatacttgt ggtgaactca agcatgttta atccaactcc atcgtctctc
 gcgatggtcg ttaacacttt caagctccga agcaacgtaa gaagctttaa
 ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
 aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
 gagaacatca cttataacat ttacgctggg gataataggt ccatgatggg
 ttcaaattgc ttgttcogtg ttggtggggc cgctattttg ctctccaaca
 agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttoga
 acgcataccg gagctgacgg caagtctttt cgttgcgtgc aacaaggaga
 cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
 ttgctggtcg aacggttaag aaaaacatag caacgttggg tccgttgatt
 cttccgttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
 acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
 ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
 ctagagaaga acctagccct agcaccgatc gatgtagagg catcaagatc
 aacgttacat agatttgga acacttcac tagctcaata tggatgagt
 tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
 cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
 tctaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
 acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
 gtcccaaacg gtcggtccta a

FIGURE 2-6

At114 K92R (SEQ ID NO:13)

```

atgacgtccg ttaacgttaa gctcctttac cgttatgtct taaccaactt
tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
ctcggtttac cataaacgat ctccacaact tcctttccta tctccaacac
aaccttataa cagtaacttt actctttgct ttcactgttt tcggtttggg
totctacatc gtaaccgcac ccaatccggg ttatctcggt gactactcgt
gttaccttcc gccaccgcat ctcaagagta gtgtctctaa agtcatggat
atcttctacc aaataagaaa agctgatact tcttcacgga acggcacgtg
tgatgattcg tcgtggcctg acttcttgag gaagattcaa gaacgttcag
gtctaggcga tgaaactcac gggcccaggg ggctgcttca ggtccctccc
cggaagactt ttgcggcggc gcgtgaagag acggagcaag ttatcattgg
tgcgctagaa aatctattca agaacaccaa cgttaacctt aaagatatag
gtatacttgt ggtgaactca agcatgttta atccaactcc atcgctctcc
gcgatggtcg ttaacacttt caagctccga agcaacgtaa gaagctttaa
ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
gagaacatca cttataacat ttacgctggg gataataggt ccatgatggg
ttcaaattgc ttgttcogtg ttggtggggc cgctatcttg ctctccaaca
agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttoga
acgcataccg gagctgacgg caagtctttt cgttgcgtgc aacaaggaga
cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
ttgctggtcg aacggttaag aaaaacatag caacgttggg tccgttgatt
cttcogttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
ctagagaaga acctagccct agcaccgatc gatgtagagg catcaagatc
aacgttacat agatttgga acacttcac tagctcaata tggatgagt
tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
totaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
gtcccaaacg gtcggtccta a

```

FIGURE 2-7

At114 G307D (SEQ ID NO:15)

atgacgtccg ttaacgttaa gctcctttac cgttatgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctcggtttac cataaacgat ctccacaact tcctttccta tctccaacac
 aacottataa cagtaacttt actctttgct ttcactgttt tcggtttggt
 tctctacatc gtaacccgac ccaatccggt ttatctcggt gactactcgt
 gttaccttcc gccacggcat ctcaaagtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acggcacgtg
 tgatgattcg tcgtggcttg acttcttgag gaagattcaa gaacgttcag
 gtctaggcga tgaaactcac gggcccaggg ggctgcttca ggtccctccc
 cggagactt ttgcggcggc gcgtgaagag acggagcaag ttatcattgg
 tgogctagaa aatctattca agaacaccaa cgttaacct aaagatatag
 gtatacttgt ggtgaactca agcatgttta atccaactcc atcgctctcc
 gogatggtcg ttaacacttt caagctccga agcaacgtaa gaagctttaa
 ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
 aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
 gagaacatca cttataacat ttacgttgtt gataataggt ccatgatggt
 ttcaaattgc ttgttccgtg ttggtggggc cgctattttg ctctccaaca
 agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
 acgcatacgg gagctgacga caagtctttt cgttgcgtgc aacaaggaga
 cgatgagAAC ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
 ttgctggtcg aacggttaag aaaaacatag caacggtggg tccgttgatt
 cttccgttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
 actttttcaa gataaaatca aacattacta cgtcccggat ttcaaacttg
 ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
 ctagagaaga acctagccct agcacccatc gatgtagagg catcaagatc
 aacgttacat agatttgga acacttcac tagctcaata tggatgagt
 tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
 cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
 tctaaacaat gtcaaagott cgacaaatag tccttgggaa cactgcacgc
 acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
 gtccaaaacg gtcggtccta a

FIGURE 2-8

At74 G306D (SEQ ID NO:17)

atgacgtccg ttaacgttaa gtccttttac cgttacgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctccggttac cataaacgat ctccacaact tcctttccta tctccaacac
 aacottataa cagtaacttt actctttgct ttcactgttt tcggtttggg
 tctctacatc gtaaccggac ccaaaccggg ttacctcggt gagtactcat
 gctaccttcc accaacgcac tgtagatcaa gtatctccaa ggtcatggat
 atcttttatc aagtaagaaa agctgatcct tctcggaacg gcacgtgcga
 tgactcgctg tggcttgact tcttgaggaa gattcaagaa cgttcaggtc
 taggcgatga aactcacggg ccgagggggc tgcttcaggc cctccccgg
 aagacttttg cggcggcgcg tgaagagacg gagcaagtta tcattgggtg
 gctagaaaat ctattcaaga acaccaacgt taaccctaaa gatataggta
 tacttggtgg gaactcaagc atgttttaac caactccatc gctctccgcg
 atggctcgta acactttcaa gctccgaagc aacgtaagaa gctttaacct
 tgggtggcatg ggttgtagtg ccggcggtat agccattgat ctagcaaagg
 acttggtgca tgtccataaa aatacgtatg ctcttggtgg gagcacagag
 aacatcactt ataacattta cgctggtgat aatagggtcca tgatggtttc
 aaattgcttg ttccgtgttg gtggggccgc tattttgctc tccaacaagc
 ctggagatcg tagacgggtc aagtacgagc tagttcacac ggttcgaacg
 cataccggag ctgacgacaa gtcttttctg tgctgcaac aaggagacga
 tgagaacggc aaaatcggag tgagtttgct caaggacata accgatgttg
 ctggtcgaac ggtaagaaa aacatagcaa cgttggtgct gttgattctt
 ccgttaagcg agaaacttct ttttttctgt accttcatgg gcaagaaact
 tttcaaagat aaaatcaaac attactacgt ccggtatttc aaacttgcta
 ttgaccattt ttgtatacat gccggaggca gagccgtgat tgatgtgcta
 gagaagaacc tagccctagc accgatcgat gtagaggcat caagatcaac
 gttacataga tttggaaaca ctcatctag ctcaatatgg tatgagttgg
 catacataga agcaaaagga aggatgaaga aaggtaataa agtttggcag
 attgcttttag ggtcaggctt taagtgtaac agtgcagttt ggggtggctct
 aaacaatgtc aaagcttcga caaatagtcc ttgggaacac tgcacgcaca
 gataccgggt caaaattgat tctgattcag gtaagtcaga gactcgtgct
 caaacgggtc ggtcctaa

FIGURE 2-9

At114 L91C K92R G307D (SEQ ID NO:19)

```

atgacgtccg ttaacgttaa gctcctttac cgttatgtct taaccaactt
tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
ctcggcttac cataaacgat ctccacaact tcctttccta tctccaacac
aaccttataa cagtaacttt actccttgct ttcactgttt tcggtttggt
tctctacatc gtaaccgac ccaatccggt ttatctcggt gactactcgt
gttaccttcc gccaccgcat tgacagagta gtgtctctaa agtcatggat
atcttctacc aaataagaaa agctgatact tcttcacgga acggcacgtg
tgataattcg tcgtggcttg acttcttgag gaagattcaa gaacgttcag
gtctaggcga tgaaactcac gggcccagg ggctgcttca ggtccctccc
cggaagactt ttgcggcggc gcgtgaagag acggagcaag ttatcattgg
tgcgctagaa aatctattca agaacaccaa cgttaaccct aaagatatag
gtatacttgt ggtgaactca agcatgttta atccaactcc atcgctctcc
gcgatggctg ttaacacttt caagctccga agcaacgtaa gaagctttaa
ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
gagaacatca cttataacat ttacgctggg gataataggt ccatgatggt
ttcaaattgc ttgttccgtg ttggtggggc cgctatcttg ctctccaaca
agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
acgcataccg gagctgacga caagtccttt cgttgcgtgc aacaaggaga
cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
ttgctggctg aacggttaag aaaaacatag caacgttggg tccgttgatt
cttccgttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
ctagagaaga acctagccct agcaccgatc gatgtagagg catcaagatc
aacgttacat agatttgaa acacttcac tagctcaata tggatgagt
tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
tctaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
gtccaaaacg gtcggtccta a

```

FIGURE 2-10

At114 K92R G307D (SEQ ID NO:21)

atgacgtccg ttaacgttaa gctcctttac cgttatgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctcggttac cataaacgat ctccacaact tcctttccta tctccaacac
 aacctataa cagtaacttt actctttgct ttcaactgttt tcggtttggt
 tctctacatc gtaacccgac ccaatccggt ttatctcggt gactactcgt
 gttaccttcc gccaccgcat ct**caga**gtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acggcacgtg
 tgatgattcg tcgtggcttg acttcttgag gaagattcaa gaacgttcag
 gtctaggcga tgaaactcac gggcccaggg ggctgcttca ggtccctccc
 cggaagactt ttgcgggcgc gcgtgaagag acggagcaag ttatcattgg
 tgcgctagaa aatctattca agaacaccaa cgttaaccct aaagatatag
 gtatacttgt ggtgaactca agcatgttta atccaactcc atcgtctctc
 gcgatggctg ttaacacttt caagctccga agcaacgtaa gaagctttaa
 ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
 aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
 gagaacatca cttataacat ttacgctggg gataataggc ccatgatggg
 ttcaaattgc ttgttccgtg ttggtggggc cgctattttg ctctccaaca
 agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
 acgcataccg gagctgac**ga** caagtctttt cgttgcgtgc aacaaggaga
 cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
 ttgctggctg aacggttaag aaaaacatag caacgttggg tccgttgatt
 cttccgttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
 acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
 ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
 ctagagaaga acctagccct agcaccgatc gatgtagagg catcaagatc
 aacgttacat agatttggaa acacttcac tagctcaata tggatatgag
 tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
 cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
 tctaaacaat gtcaaaagct cgacaaatag tccttgggaa cactgcacgc
 acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
 gtccaaaacg gtcggtccta a

FIGURE 2-11

At254 (SEQ ID NO:23)

atgacgtccg ttaacgttaa gctcctttac cgttacgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctcggttac cataaacgat ctccacaacc tcctttccta tctccaacac
 aaccttataa cagtaacttt actctttgct ttcaactgttt tcgggttggt
 totctacatc gtaacccgac ccaatccggt ttatctcggt gactactcgt
 gttaccttcc accaccgcat ctcaaagtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg
 tgatgatccg tcctcgctcg atttcctgag gaagattcaa gagcgttcag
 gtctaggtga tgagacgtac agtcctgagg gactcattca cgtaccaccg
 cggaaagactt ttgcagcgtc acgtgaagag acagagaagg ttatcatcgg
 tgcgctcgaa aatctattcg agaacaccaa agttaaccct agagagattg
 gtatacttgt ggtgaactca agcatgttta atccaactcc ttcgctatcc
 gctatggctg ttaatacttt caagctccga agcaacatca aaagctttaa
 totaggagga atgggttgta gtgctggtgt tattgccatt gatttggtca
 aagacttggt gcatgttcat aaaaacactt atgctctcgt ggtgagcaca
 gagaacatca cttataacat ttacgctggt gataataggt ccatgatggt
 ttcaaattgc ttgttcctg ttggtggggc cgctattttg ctctccaaca
 agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
 acgcataccg gagctgacgg caagtctttt cgttgcgtgc aacaaggaga
 cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
 ttgctggctg aacgggttaag aaaaacatag caacggtggg tccggtgatt
 cttccgttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
 acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
 ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
 ctagagaaga acctagccct agcaccgatc gatgtagagg catcaagatc
 aacgttacat agatttgga acacttcac tcagctcaata tgggtatgagt
 tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
 cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
 totaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
 acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
 gtcccaaacg gtcgggtccta a

FIGURE 2-12

At173 (SEQ ID NO:25)

atgacgtccg ttaacgttaa gtccttttac cgttacgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctgggttac cataaacgat ctccacaact tcctttccta tctccaacac
 aacctataa cagtaacttt actctttgct ttcactgttt tcggtttggg
 tctctacatc gtaacccgac ccaatccggt ttatctcggt gactactcgt
 gttaccttcc accaccgcat ctcaaagtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg
 tgatgatccg tcctcgctcg atttcttgag gaagattcaa gagcgttcag
 gtctaggtga tgagacgtac agtcctgagg gactcattca cgtaccaccg
 cggaagactt ttgcagcgtc acgtgaagag acagagaagg ttatcatcgg
 tgcgctcgaa aatctattca agaacaccaa cgttaaccct aaagatatag
 gtatacttgt ggtgaactca agcatgttta atccaactcc atcgctctcc
 gcgatggctg ttaacacttt caagctccga agcaacgtaa gaagctttaa
 ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
 aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
 gagaacatca cttataacat ttacgtgggt gataataggt ccatgatggg
 ttcaaattgc ttgttccgtg ttggtggggc cgtatattttg ctctccaaca
 agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
 acgcataccg gagctgacgg caagtctttt cgttgcgctgc aacaaggaga
 cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
 ttgotggctg aacggttaag aaaaacatag caacggtggg tccgttgatt
 ctccggttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
 acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
 ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
 ctagagaaga acctagccct agcacccgac gatgtagagg catcaagatc
 aacgttacat agatttgga acaacttcac tagctcaata tggatatgag
 tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
 cagattgctt tagggctcagg ctttaagtgt aacagtgcag tttgggtggc
 tctaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
 acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
 gtccaaaacg gtcggtccta a

FIGURE 2-13

Bn176 (SEQ ID NO:27)

atgacgtcca ttaacgtaaa gctcctttac cattacgtca taaccaacct
 tttcaacctt tgcttctttc cgttaacggc gatcgtcgcc ggaaaagcct
 atcggcttac catagacgat cttcaccact tatactattc ctatctccaa
 cacaacctca taaccatcgc tccactcttt gccttcacgg ttttcggttc
 ggtttctctac atcgcaaccc ggcccaaacc ggtttacctc gttgagtact
 catgctacct tccaccaacg cattgtagat caagtatctc caaggtcattg
 gatattcttt atcaagtaag aaaagctgat ccttctcgga acggcacgtg
 cgatgactcg tcgtggcttg acttcttgag gaagattcaa gaacgttcag
 gtctaggcga tgaaactcac gggcccgagg ggcgtgcttc ggtccctccc
 cggagactt ttgcggcggc gcgtgaagag acggagcaag ttatcattgg
 tgcgctagaa aatctattca agaacaccaa agttaacct agagagattg
 gtatacttgt ggtgaactca agcatgttta atccaactcc ttcgctatcc
 gctatggctg ttaatacttt caagctccga agcaacatca aaagctttaa
 tctaggagga atgggttgta gtgctgggtg tattgccatt gatttggcta
 aagacttggt gcatgttcat aaaaacactt atgctcttgt ggtgagcact
 gagaacatca cacaaggcat ttatgctgga gaaaatagat caatgatggg
 tagcaattgc ttgtttcgtg ttggtggggc cgcgattttg ctctctaaca
 agtcgggaga cgggagacgg tccaagtaca agctagtcca cacggtcoga
 acgcatactg gagctgatga caagtctttt cgatgtgtgc aacaagaaga
 tgatgagagc ggcaaaatcg gagtttgtct gtcaaaggac ataaccaatg
 ttgcggggac aacacttacg aaaaatatag caacattggg tccgttgatt
 cttcctttaa gcgaaaagtt tcttttttct gctaccttcg tcgccaagaa
 acttctaaag gataaaatca agcattacta tggtccggat ttcaagcttg
 ctgttgacca tttctgtatt catgccggag gcagagccgt gatcgatgag
 ctagagaaga acttaggact atcgccgac gatgtggagg catctagatc
 aacgttacat agatttgga atacttcac tagctcaatt tggatgaat
 tagcatacat agaggcaaag ggaagaatga agaaagggaa taaagcttgg
 cagattgctt taggatcagg gtttaagtgt aatagtgcgg tttgggtggc
 tctacgcaat gtcaaggcat cggcaaatag tccttggcaa cattgcatcg
 atagatatcc ggttaaaatt gattctgatt tgtcaaagtc aaagactcat
 gtccaaaacg gtcggtccta a

FIGURE 2-14

At399 (SEQ ID NO:29)

atgacgtccg ttaacgttaa gctcctttac cgttacgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctgggcttac cataaacgat ctccacaact tcctttccta tctccaacac
 aaccttataa cagtaacttt actctttgct ttcaactgttt tcggtttggt
 tctctacatc gtaaccgac ccaatccggt ttatctcggt gactactcgt
 gttaccttcc accaccgat ctcaaagtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg
 tgatgatccg tctcgctcg atttctgag gaagattcaa gagcgttcag
 gtctagggtga tgagacgtac agtctgagg gactcattca cgtaccaccg
 cggagactt ttgcagcgtc acgtgaagag acagagaagg ttatcatcgg
 tgogctcgaa aatctattcg agaacaccaa agttaaccct agagagattg
 gtatacttgt ggtgaactca agcatgttta atccaaactcc ttcgctatcc
 gctatggctg ttaatacttt caagctccga agcaacatca aaagctttaa
 tctaggagga atgggttgta gtgctggtgt tattgccatt gatttggtta
 aagacttggt gcatgttcat aaaaacactt atgctcttgt ggtgagcact
 gagaacatca cacaaggcat ttatgctgga gaaaatagat caatgatggt
 tagcaattgc ttgtttcgtg ttggtggggc cgcgattttg ctctctaaca
 agtcgggaga cgggagacgg tccaagtaca agctagtcca cacggtcoga
 acgcatactg gagctgatga caagtctttt cgatgtgtgc aacaagaaga
 cgatgagagc ggcaaaatcg gagtttgtct gtcaaaggac ataaccaatg
 ttgcggggac aacacttacg aaaaatatag caacattggg tccgttgatt
 cttcctttaa gcgaaaagtt tctttttttc gctaccttcg tcgccaagaa
 acttctaaag gataaaatca agcattacta tgttccggat ttcaagcttg
 ctggtgacca tttctgtatt catgccggag gcagagccgt gatcgatgtg
 ctagagaaga acctagccct agcaccgatc gatgtagagg catcaagatc
 aacgttacat agatttgga acacttcac tagctcaata tggatgagt
 tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
 cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
 tctaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
 acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
 gtccaaaacg gtcggtccta a

FIGURE 2-15

Bn399 (SEQ ID NO:31)

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atgacgtcca ttaacgttaa gctcctttac cattacgtca taaccaacct
tttcaacctt tgcttctttc cgttaacggc gatcgtcgcc ggaaaagcct
atcggttac catagacgat cttcaccact tatactattc ctatctccaa
cacaacctca taaccatcgc tccactcttt gccttcaccg ttttcggttc
ggttctctac atcgcaaccc ggcccaaacc ggtttacctc gttgagtact
catgctacct tccaccaacg cattgtagat caagtatctc caaggtcatg
gatatctttt atcaagtaag aaaagctgat ccttctcggg acggcacgtg
cgatgactcg tcgtggcttg acttcttgag gaagattcaa gaacgttcag
gtctaggcga tgaaactcac gggcccagag ggctgcttca ggtccctccc
cggaagactt ttgcggcggc gcgtgaagag acggagcaag ttatcattgg
tgcgctagaa aatctattca agaacaccaa cgttaacctt aaagatatag
gtatacttgt ggtgaactca agcatgttta atccaactcc atcgctctcc
gcgatggctg ttaacacttt caagctccga agcaacgtaa gaagctttaa
ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
gagaacatca cttataacat ttacgctggg gataataggt ccatgatggg
ttcaaattgc ttgttcctg ttggtggggc cgtattttg ctctccaaca
agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
acgcataccg gagctgaagg caagtctttt cgttgctgc aacaaggaga
cgatgagaac ggcaaaatcg gagtgaagtt gtccaaggac ataaccgatg
ttgctggctg aacggttaag aaaaacatag caacgttggg tccgttgatt
cttcctgtaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
ctattgacca tttttgtata catgccggag gcagagccgt gatcgatgag
ctagagaaga acttaggact atcgccgac gatgtggagg catctagatc
aacgttacat agatttggga atacttcac tagctcaatt tggatgaat
tagcatatat agaggcaaag ggaagaatga agaaagggaa taaagcttgg
cagattgctt taggatcagg gtttaagtgt aatagtgcgg tttgggtggc
tctacgcaat gtcaaggcat cggcaaatag tcottggcaa cattgcatcg
atagatatcc ggttaaaatt gattctgatt tgtcaaagtc aaagactcat
gtccaaaacg gtcggtccta a

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FIGURE 2-16

Bn G307D (SEQ ID NO:33)

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atgacgtcca ttaacgtaaa gctcctttac cattacgtca taaccaacct
tttcaacctt tgcttctttc cgttaacggc gatcgtcgcc ggaaaagcct
atcggcttac catagacgat cttcaccact tatactatcc ctatctccaa
cacaacctca taaccatcgc tccactcttt gccttcacccg ttttcggttc
ggttctctac atcgcaaccc ggcccaaacc ggtttacctc gttgagtact
catgctacct tccaccaacg cattgtagat caagtatctc caaggtcatg
gatatctttt atcaagtaag aaaagctgat ccttctcggg acggcacgtg
cgatgactcg tcgtggcttg acttcttgag gaagattcaa gaacgttcag
gtctaggcga tgaaactcac gggcccaggg ggctgcttca ggtccctccc
cggaagactt ttgcggcggc gcgtgaagag acggagcaag ttatcattgg
tgcgctagaa aatctattca agaacaccaa cgttaaccct aaagatatag
gtatacttgt ggtgaactca agcatgttta atccaactcc atcgctctcc
gogatggctg ttaacacttt caagctccga agcaacgtaa gaagctttaa
ccttggtggc atggggttga gtgccggcgt tatagccatt gatctagcaa
aggacttggt gcattgtccat aaaaatacgt atgctcttgt ggtgagcaca
gagaacatca cttataacat ttacgctggg gataataggt ccatgatggg
ttcaaattgc ttgttcctgt ttggtggggc cgctattttg ctctccaaca
agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
acgcataccg gagctgacga caagtctttt cgttgctgctc aacaaggaga
cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
ttgctggctg aacggttaag aaaaacatag caacgttggg tccgttgatt
cttccgttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
ctagagaaga acctagccct agcaccgatc gatgtagagg catcaagatc
aacggtacat agatttgga acacttcac tagctcaata tggtagagt
tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
tctaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
gtccaaaacg gtcggtccta ataa

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FIGURE 2-17

At K92R (SEQ ID NO:35)

atgacgtccg ttaacgttaa gctcctttac cgttacgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctoggcttac cataaacgat ctccacaact tcctttccta tctccaacac
 aaocctataa cagtaacttt actctttgct ttcactgttt tcggtttggt
 tctctacatc gtaaccggac ccaatccggt ttatctcggt gactactcgt
 gttaccttcc accaccgcat ctc**ag**agtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg
 tgatgatccg tcctcgctcg atttctgag gaagattcaa gaggcttcag
 gtctagggtga tgagacgtac agtcctgagg gactcattca cgtaccaccg
 cggagactt ttgcagcgtc acgtgaagag acagagaagg ttatcatcgg
 tgcgctcgaa aatctattcg agaacaccaa agttaaccct agagagattg
 gtatacttgt ggtgaactca agcatgttta atccaactcc tcgctatcc
 gctatggctg ttaatacttt caagctccga agcaacatca aaagctttaa
 tctaggagga atgggttgta gtgctggtgt tattgccatt gatttggtta
 aagacttggt gcatgttcat aaaaacactt atgctcttgt ggtgagcact
 gagaacatca cacaaggcat ttatgctgga gaaaatagat caatgatggt
 tagcaattgc ttgtttcgtg ttggtggggc cgggattttg ctctctaaca
 agtcggggaga cgggagacgg tccaagtaca agctagttca cacggtccga
 acgcatactg gagctgatga caagtctttt cgatgtgtgc aacaagaaga
 cgatgagagc ggcaaaatcg gagtttgtct gtcaaaggac ataaccaatg
 ttgcggggac aacacttacg aaaaatatag caacattggg tccgttgatt
 ctctctttaa gcgaaaagtt tcttttttct gctaccttcg tcgccaagaa
 acttctaaag gataaaatca agcattacta tgttcgggat ttcaagcttg
 ctgttgacca tttctgtatt catgccggag gcagagccgt gatcgatgag
 ctagagaaga acttaggact atcgccgac gatgtggagg catctagatc
 aacgttacat agatttggga atacttcac tagctcaatt tggatgaat
 tagcatacat agaggcaaag ggaagaatga agaaagggaa taaagcttgg
 cagattgctt taggatcagg gtttaagtgt aatagtgcgg ttgggtggc
 tctacgcaat gtcaaggcat cggcaaatag tccttggcaa cattgcacg
 atagatatcc ggttaaaatt gattctgatt tgtcaaagtc aaagactcat
 gtccaaaacg gtcggtccta atttgatgta tctgagtgc aacgtttact
 ttgtctttcc tttcttttat tggttatgaa ttagatgttt actaatgttc
 ctctcttttt cgttataaat aaagaagttc aattcttct atagtttcaa
 acgcgatttt aagcgtttct atttaggttt acatgaattt cttttacaaa
 ccatotttt

FIGURE 2-18

At254 G307D (SEQ ID NO:37)

atgacgtccg ttaacgttaa gctcctttac cgttacgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctgggcttac cataaacgat ctccacaact tcctttccta tctccaacac
 aaccttataa cagtaacttt actctttgct ttcaactgttt tcgggttggt
 totctacatc gtaaccogac ccaatccggg ttatctcggt gactactcgt
 gttaccttcc accaccgcat ctcaaagtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg
 tgatgatccg tcctcgctcg atttctgag gaagattcaa gagcggtcag
 gtctaggtga tgagacgtac agtcctgagg gactcattca cgtaccaccg
 cggaagactt ttgcagcgtc acgtgaagag acagagaagg ttatcatcgg
 tgcgctcgaa aatctattcg agaacaccaa agttaaccct agagagattg
 gtatacttgt ggtgaactca agcatgttta atccaactcc ttcgctatcc
 gctatggtcg ttaatacttt caagctccga agcaacatca aaagctttaa
 tctaggagga atgggttgta gtgctggtgt tattgccatt gatttggcta
 aagacttggt gcatgttcat aaaaacactt atgctctcgt ggtgagcaca
 gagaacatca cttataacat ttacgctggt gataataggt ccatgatggt
 ttcaaattgc ttgttccgtg ttggtggggc cgctattttg ctctccaaca
 agcctggaga tcgtagacgg tccaagtacg agctagtcca cacgggttga
 acgcataccg gagctgacga caagtctttt cgttgctgac aacaaggaga
 cgatgagaac ggcaaaatcg gagtgaagtt gtccaaggac ataaccgatg
 ttgctggtcg aacggttaag aaaaacatag caacggtggg tccggttgatt
 cttccgttaa gcgagaaact tctttttttc gttacottca tgggcaagaa
 acttttcaaa gataaaatca aacattacta cgtcccggtt ttcaaacttg
 ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
 ctagagaaga acctagccct agcaccgatc gatgtagagg catcaagatc
 aacggttacat agatttgga acacttcatc tagctcaata tggatgagt
 tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
 cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
 tctaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
 acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
 gtccaaaacg gtccgtccta a

FIGURE 2-19

At173 G307D (SEQ ID NO:39)

atgacgtccg ttaacgttaa gtccttttac cgttacgtct taaccaactt
 tttcaacctc tgtttggtcc cgttaacggc gttcctcgcc ggaaaagcct
 ctccggttac cataaacgat ctccacaact tcctttccta tctccaacac
 aacottataa cagtaacttt actctttgct ttcactgttt tcggtttggg
 tctctacatc gtaaccgcac ccaatccggg ttatctcggt gactactcgt
 gttaccttcc accaccgcac ctcaaagtta gtgtctctaa agtcatggat
 attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg
 tgatgatccg tctcgcctcg atttccctgag gaagattcaa gagcgttcag
 gtctaggtga tgagacgtac agtcctgagg gactcattca cgtaccaccg
 cggagactt ttgcagcgtc acgtgaagag acagagaagg ttatcatcgg
 tgccgtcga aatctattca agaacaccaa cgtaaccct aaagatatag
 gtatacttgt ggtgaactca agcatgttta atccaactcc atcgcctctc
 gcgatggtcg ttaacacttt caagctccga agcaacgtaa gaagctttta
 ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
 aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
 gagaacatca cttataacat ttacgctggg gataataggt ccatgatggg
 ttcaaattgc ttgttcctg ttggtggggc cgtatatttg ctctccaaca
 agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
 acgcataccg gagctgacga caagtctttt cgttgctgc aacaaggaga
 cgatgagaac ggcaaaatcg gaggtagttt gtccaaggac ataaccgatg
 ttgctggtcg aacggttaag aaaaacatag caacggtggg tccgttgatt
 cttccgttaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
 acttttcaaa gataaaatca aacattacta cgtcccggat ttcaaacttg
 ctattgacca tttttgtata catgccggag gcagagccgt gattgatgtg
 ctagagaaga acctagccct agcacgcgac gatgtagagg catcaagatc
 aacgttacat agatttgga acaacttcac tagctcaata tggatgagt
 tggcatacat agaagcaaaa ggaaggatga agaaaggtaa taaagtttgg
 cagattgctt tagggtcagg ctttaagtgt aacagtgcag tttgggtggc
 tctaaacaat gtcaaagctt cgacaaatag tccttgggaa cactgcacgc
 acagataccc ggtcaaaatt gattctgatt caggtaagtc agagactcgt
 gtccaaaacg gtcggtccta a

FIGURE 2-20

Bn399 G307D (SEQ ID NO:41)

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atgacgtcca ttaacgttaa gctcctttac cattacgtca taaccaacct
tttcaacctt tgcttctttc cgttaacggc gatcgtcgcc ggaaaagcct
atcggcttac catagacgat cttcaccact tatactattc ctatctccaa
cacaacctca taaccatcgc tccactcttt gccttcaccg ttttcggttc
ggttctctac atcgcaaccc ggcccaaacc ggtttacctc gttgagtact
catgctacct tccaccaacg cattgtagat caagtatctc caaggtcatg
gatatctttt atcaagtaag aaaagctgat ccttctcgga acggcacgtg
cgatgactcg tcgtggcttg acttcttgag gaagattcaa gaacgttcag
gtctaggcga tgaaactcac gggcccagag ggctgcttca ggtccctccc
cggaagactt ttgcgggcggc gcgtgaagag acggagcaag ttatcattgg
tgcgctagaa aatctattca agaacaccaa cgttaaccct aaagatatag
gtatacttgt ggtgaactca agcatgttta atccaactcc atcgctctcc
gcgatggctg ttaacacttt caagctccga agcaacgtaa gaagctttaa
ccttggtggc atgggttgta gtgccggcgt tatagccatt gatctagcaa
aggacttggt gcatgtccat aaaaatacgt atgctcttgt ggtgagcaca
gagaacatca cttataacat ttacgctggg gataataggt ccatgatggg
ttcaaattgc ttgttcctg ttggtggggc cgctattttg ctctccaaca
agcctggaga tcgtagacgg tccaagtacg agctagtcca cacggttcga
acgcataccg gagctgacga caagtctttt cgttgctgctc aacaaggaga
cgatgagaac ggcaaaatcg gagtgagttt gtccaaggac ataaccgatg
ttgctggctg aacggttaag aaaaacatag caacgttggg tccgttgatt
cttcctgtaa gcgagaaact tctttttttc gttaccttca tgggcaagaa
actttttcaa gataaaatca aacattacta cgtcccggat ttcaaacttg
ctattgacca tttttgtata catgccggag gcagagccgt gatcgatgag
ctagagaaga acttaggact atcgccgac gatgtggagg catctagatc
aacgttacat agatttgga atacttcac tagctcaatt tggatgaat
tagcatacat agaggcaaag ggaagaatga agaaagggaa taaagcttgg
cagattgctt taggatcagg gtttaagtgt aatagtgcgg tttgggtggc
tctacgcaat gtcaaggcat cggcaaatag tccttggcaa cattgcatcg
atagatatcc gggtaaaatt gattctgatt tgtcaaagtc aaagactcat
gtccaaaacg gtcggtccta a

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FIGURE 2-21